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December 23, 2004, 12:22:29; Search time 826 Seconds (without alignments) 10524.263 Million cell updates/sec
                                                                                                                                                                                                                                1 aagtaatatcacaatagsgg......ggtgttkggaaraaataacg 1656
                                                                                                                                                                                                                                                                                                                                                                   8269772
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         4134886 segs, 2624710521 residues
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Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1: geneseqn1980s:*
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1656
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |       | •     |                 |    | SUMMARIES               |                    |
|--------|-------|-------|-----------------|----|-------------------------|--------------------|
| Result |       | Query |                 |    |                         |                    |
| No.    | Score | Match | Match Length DB | 80 | QI.                     | Description        |
| п      | 292.4 | 17.7  | 110000          | 7  | AAT42063 09             | Continuation (10 o |
| 7      | 197.8 | 11.9  | 1572            | m  | AAA15298                | Aaa15298 DNA encod |
| e      | 196.2 | 11.8  | 1575            | ~  | AAZ12105                | Aaz12105 Neisseria |
| 4      | 196.2 | 11.8  | 12438           | m  | AAA81550                | Aaa81550 N. mening |
| 'n     | 196.2 | 11.8  | 110000          | m  | AAA81489 6              | Continuation (7 of |
| 9      | 196.2 | 11.8  | 172325          | ო  | AAF21613                | Aaf21613 Neisseria |
| 7      | 196.2 | 11.8  | 349980          | m  | AAF21612                | Aaf21612 Neisseria |
| 80     | 185.8 | 11.2  | 1467            | 10 | ABZ41628                | Abz41628 N. gonorr |
| σ      | 185.8 | 11.2  | 1575            | N  | AAZ12107                | Aaz12107 Neisseria |
| 10     | 185.8 | 11.2  | 1575            | m  | AAA15323                | Aaa15323 DNA encod |
| 11     | 120.8 | 7.3   | 1275            | ~  | AAZ12106                | Aaz12106 Neisseria |
| 12     | 96.6  | 5.8   | 110000          | 10 | ACF65385 0              | Acf65385 Photorhab |
| 13     | 9.96  | 5.8   | 110000          | 10 | ACF67367 <sup>2</sup> 9 | Continuation (30 o |
| 14     | 95.4  | 5.8   | 1284            | 10 | ACF69918_               | Acf69918 Photorhab |
| 15     | 95.4  | 5.8   | 1335            | σ  | ADA31630                | Ada31630 DNA encod |
| 16     | 91.4  | 5.5   | 47108           | 9  | ABK31510                | Abk31510 Signal tr |
| 17     | 89.4  | 5.4   |                 | 80 | AB210246                | Abz10246 Haematopo |
| 18     | 88.2  | 5.3   | 1377            | 11 | ABD11809                | Abd11809 Pseudomon |
| 19     | 88.2  | 5.3   | 1383            | 11 | ABD11702                | Abd11702 Pseudomon |
| c 20   | 88.2  | 5.3   | 1410            | 1  | ABD12145                | Abd12145 Pseudomon |
| 21     | 87.2  | 5.3   | 19380           | v  | AAS61427                | Aas61427 Human gen |

| Ab192313 Chemicall<br>Aag46530 Timour gu | Abz10199 Haematopo | Adb54225 Pretreate | Ade84163 Human lym | Abl32960 Human imm | Abz10100 Haematopo | Abk40068 Human che | Abl33096 Human imm | Abk40056 Human che | Abl32267 Human imm | Abl34174 Human imm | Abz10246 Haematopo | Abl33697 Human imm | Acf62816 Colon can | Adb54318 Pretreate | Aas45323 Chemicall | Abk39976 Human che | Abk28164 DNA trans | Abz10053 Haematopo | Aas46743 Tumour su | Abk33955 Human DNA | Ada20386 Prostate | Ada84193 Human ren |
|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| 6 ABL92313                               | 8 ABZ10199         | 10 ADB54225        | 10 ADE84163        | 6 ABL32960         | 8 ABZ10100         | 6 ABK40068         | 6 ABL33096         | 6 ABK40056         | 6 ABL32267         | 6 ABL34174         | 8 ABZ10246         | 6 ABL33697         | 8 ACF62816         | 10 ADB54318        | 4 AAS45323         | 6 ABK39976         | 6 ABK28164         | 8 ABZ10053         | 4 AAS46743         | 6 ABK33955         | 8 ADA20386        | 8 ADA84193         |
| .2 8079<br>2 7814                        | .2 3683            | .1 14147           | .1 14147           | .1 6255            | .1 8056            | 9228 0.            | 5.0 5822           | _                  | 5.0 6419           | .0 113515          | 9508 0.            | .9 6668            | .9 8222            | .9 11222           | .9 17848           | .9 17848           | .9 17848           | .9 3683            | .9 14147           | .9 14147           | .9 14147          | .9 14147           |
| 86.6                                     | 85.6 5             | 84.4 5             | 84.4 5             | 84.2 5             | 83.8 5             |                    | 83.4 5             |                    |                    | 82.8 5             | 82.2 5             | 81.8 4             | 81.8 4             | 81.8 4             | 81.4 4             | 81.4 4             | 81.4 4             | 81.2 4             | 81.2 4             | 81.2 4             | 81.2 4            | 81.2 4             |
| 22                                       | 24                 | 25                 | 56                 | 27                 | c 28               | 29                 | 30                 | 31                 | 32                 | 33                 | C 34               | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                | 45                 |

## ALIGNMENTS

| E 100 P        |   |                             |   |       |     |
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| AAT42063 09    |   |                             |   |       |     |
|                |   |                             | щ   |       | ger |
| Segu           | t into 19                               |                             |   |       |     |
|                | Name                                    | Begin                       | End   |       |     |
|                | 00                                      | -                           | 110000  |       |     |
|                | 01                                      | 100001                      | 210000  |       |     |
| WP AAT42063_02 | 02                                      | 200001                      | 310000  |       |     |
|                | 03                                      | 300001                      | 410000  |       |     |
|                | 04                                      | 400001                      | 510000  |       |     |
|                | 0.5                                     | 500001                      | 610000  |       |     |
|                | 90                                      | 600001                      | 710000  |       |     |
| WP AAT42063_07 | 0.7                                     | 700001                      | 810000  |       |     |
|                | 80                                      |                             | 910000  |       |     |
| WP AAT42063    | 60                                      |                             | 1010000   |       |     |
|                |   |                             | 1110000   |       |     |
| WP AAT42063_11 |   | 11000011                    | 1210000   |       |     |
| WP AAT42063    |   |                             | 1310000   |       |     |
|                |   |                             | 1410000   |       |     |
| AAT42063       |   |                             | 1510000   |       |     |
|                | 15                                      |                             | 1610000   |       |     |
| WP AAT42063_16 | 16                                      |                             | 1710000   |       |     |
|                | 17                                      |                             | 1810000   |       |     |
| WP AAT42063_18 | 18                                      | 1800001                     | 1830121   |       |     |
| Match Watch    |   | 17 78. 6                    | Score 292 4: DB 2: Length 110000:                               |       |     |
| Query marcin   | 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 |                             | 10-05   |       |     |
| Matches 336;   | Similarity 85.                          | 14;                         | Mismatches 57; Indels 1; Gaps                                   | 1,    |     |
| Qy 8 A7        | CACAATAGS                               | GGATCCACGA                  | ATCACAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGGATATCC 6   | 67    |     |
|                |   |                             |   |       |     |
| DD 41919 AT    | PATCACAATG                              | ATATCACAATGGGATCTGCGAGCTTCT | -TTAGGTATCGTATTGGCTGCAGAGGGATACCC                               | 41977 |     |
| Qy 68 AJ       | AGGATTATC                               | GCAAAGGCGA.                 | AAAGGATTATCGCAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 1  | 127   |     |
|                |   |                             |   |       |     |
| DD 41978 AZ    | AAGATTATC                               | GCAAAGGCGA                  | AAAAGATTATCGCAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 4  | 42037 |     |
| Qy 128 G       | VAAGTTTTCT                              | TAGCGGGTGT                  | GANAGTITICTTAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGTCG    | 187   |     |
| Db 42038 G     | AAGTTTTCT                               | TAGCGGGTGT                  | GAAAGTITICTIAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGTCG 4  | 42097 |     |
| Qy 188 TC      | STACTTTGTG                              | TGACTGCGTT                  | TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAACAAAAAAGCGTTAAA 2 | 247   |     |
| 000            |   |                             |   | 101   |     |
| UD 42098 TC    | TACTITION                               | TGACTGCGTT                  | TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAAAAAAGCGTTAAA 4    | / 517 |     |

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1426 TGCATATGATCAATTTTTTAGGAGGAGCTTGGATTGATGATGATTCGTTTTCCAGATAATG 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 GCCTCGCCAAAGAGCAGGCTATGAAACGTATTTTACAGCGCACAGGCGGAAAACGAGA
CTTCGCGGCTGCTGATTGCGCGTTTTTCGCGTTCAGCATTATTGCCAACAATGTACATT
                                                                                                                         ATGAGATAACAAATGCTGGCTTAACAATGATAGATAAATTCATATATCCATTGTTATTTG
                                                                                                                                                                                                                      GTTTATTTGAAGTTGCTGTGTTTTTAAGTTTTAAGTTTCATAAAAAGAAAAGTATATAAAC
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                                                                         ATGCAGTATACCAATCTTGGATTTGGACCTGTTAATTACTCACTTGCATTTAAAGAAATTA
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                                                     The present sequence encodes a protein that is specific for pathogenic strains of Neisseria. The polymucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polymucleotide sequence is also used for recombinant production of the polymeptide and to produce attenuated Neisseria strains that overexpress it, or express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cadada certric cecrea carriarie arricerecerierar creritie de certara de 169
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                                                                                                                      TGTGGAACGAGAACAAAATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pathogenic strain; Neisseria; vaccine; Neisseria infection; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a polypeptide of a Neisseria pathogenic strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INWR ) PASTEUR MERIEUX SERUMS & VACCINS SA.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                    368 ATTGTACAGGGTAGAATTGTATTTTCCTAGGATTT
                                                                                                                                                                                                                                                                    GATGAAATTTAGGAATGAAATTTTAATTAAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 197.8; D
Pred. No. 2.4e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 56-59; 187pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                        AAA15298 standard; DNA; 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-FR002643
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llarity 51.6%;
Conservative
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Perrin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis.
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Les 533; Conserv
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Tinsley C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1486 AAGGGTATTCTTTAAGAGATTCAATGCCTGATAATAAATTACTTCCTGCTTTTAAAATA 1545
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                                                                                                                                                                                                                                                                                                                                                GTTACGGGAGAAAAACATCTCCTTTTTAGATAG---CTTAAAATATAAATCAGGAGCTC 1245
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                                                                                                                                                                                           1069 TATCTAATATTCCTCTTTATCATAAATCTAAGCCTATGAAATCGGGCTCTCCGVAAAATT 1128
                                       949 ATACAACAAAATCCCATGAGCGTTTTATTTCACCTAACACTGTTTATTCTCGATTAAAAT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814
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                                                                                                                                                     577
                                                                                                                                                                                                                               634
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 457
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antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1366 ATTTAGCGAAAGAGCAAGGCTTTCAGACATATTTTTATTCAGCTCAAGCTAGGGATGATA
-----TITICIGCCGATATACTGTTTGCCTTCCTAATGCTGATGATTTTCGTGCGTT
                                                                         458 cerrceacacacaacaadaadacacecrarricecccaaaaccaacaracaeccecarcaaa
                                                                                                                 CCAATTATTTATCGTTGGGTTATTTATAGGACGAATTGTTCCTTATGAGATATTTTCTT
                                                                                                                                                                                                                               578 raacaggarricccccrrraaggagccrcrccaagcaaarcccc--caccacrc
                                                                                                                                                                                                                                                                                                          635 TTCAAAATATCGTCCTGATTATGGGCGAAAGCGAAAGCGCGGCGCATTTGAAGCTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 rigigaaacaaagriarriccecaeecrrrareacrececereccececearririca
                                                                                                                                                   ccaarratricaecricestriarrirercesacecererrecesiarearricarr
                                                                                                                                                                                                                                                                    1129 MARGAATATAATTTAATTAATGGGGGAAAGTGCGACCTCAAGTCATTTTAGTGCTTTTG
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                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229
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                                                                                                 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea;
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Pred. No. 4.6e-26;
2; Mismatches 481; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins from Neisseria meningitidis and N. gonorrhoeae diagnosis, treatment and prevention of infection.
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                                                             Neisseria meningitidis complete ORF81 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pizza M,
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97GB-00024190.
97GB-00024386.
97GB-00025158.
96GB-00000759.
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14-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                   The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseriam meningitidis genomic DNA sequences. AAA81260 to AAA81263 and AAA81265 represent Neisseria DNA sequences and their corresponding proteins; AAA81264 to AAA81259 and AAA81264 to AAA81254 to AAA81259 and AAA81264 to AAA81252 represent PCR primers used in the isolation of Neisseriam meningitidis Mons polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid used in the exemplification of the present invention. The nucleic acid used in the exemplification of the present invention. The nucleic acid the manufacture of a composition of medicament (or in the manufacture of a medicament) for treating. The manufacture of a composition of a medicament or in the manufacture of a medicament or in the manufacture of a medicament or vising infection due to Neisserial bacteria. For example, some of the identified proteins components of vaccines against Meningococcus B; againet all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have also been tried but none have successfully overcome antigent variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presenued targets for the immune system and which are not that may be presenued targets for the immune system and entered to the provision of the may or the provision of the may organism.
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                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.
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                                                                                   Tettelin H, Venter JC;
Ratti G, Scarselli M,
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2; Mismatches 481; Indels
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                                                                                                                                                                                                                                                           Claim 7; Page 1489-1492; 1760pp; English.
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                                                                                     Peterson C, Moral
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Galeotti
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Rappuoli R, Pizza M;
                                                   (CHIR ) CHIRON CORP.
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Matches 532; Conserv
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from base 600001 (N. meningitidis partial DNA sequence LOCUS AAA81489 Accession Aaa81489 End
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                                                                                                                                              769 ATGAGATAACAAATGCTGGCTTAACAATGATAGATAAATTCCATATATCCATTGTTATTTG
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AAF21613 standard; DNA; 172325 BP.

AAF21613

RESULT 6
AAF21613
ID AAF2
XX
AC AAF2

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The present invention describes the full length genome of Neisseria

meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613

crepresent fragments of the NMB genomic sequence, as the sequence was too

long to go in a record on its own it was split into 8 sequences which

coverlap each other at the beginning and end of each sequence by 49980 bp

coverlap each other at the beginning and end of each sequence by 49980 bp

coverlap each other at the beginning of the beginning of the last 49980 bp of AAF21541 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21507 are repeated at the beginning of AAF21607, and so on). AAF21545 to AAF21589 to AAF21608 represent proteins

consider the last 49980 bp of AAF21590 to AAF2160 represent proteins

consider the last 49980 bp of AAF21590 to AAF2160 represent proteins

consider the last 49980 bp of AAF21607 are repeated at the beginning of AAF21609, and so AAF21608 represent proteins

consider the last 49980 bp of AAF21607 are repeated in remonstance and gene therapy. Neisserial activity, and can be used in vaccines and gene therapy. Neisserial nucleic acids, proteins

conflor antibodies which binds to the proteins can be used in compositions

conflor antibodies raised to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or conjuter storage medium or computer databases can be used in a search to computer storage medium or computer databases can be used in a search to dentify open reading frames (ORFS) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the constant proteins currently used

couter membrane proteins currently used
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                                                                                                         Neisseria meningitidis, Neisseria gonorrheae; immunogenic, vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
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Scarselli M,
                                                              Neisseria meningitidis B nucleotide sequence SEQ ID NO:114.
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Pred. No. 6.7e-26;
2; Mismatches 481; Indels
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Ratti G,
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28-FEB-2000; 2000GB-00004695.
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Best Local Similarity 51.5%;
Matches 532; Conservative
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Rappuoli R, Frazer CM,
                                                                                                                                                                                                       Neisseria meningitidis.
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Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial; das grandes

Neisseria meningitidis.

WO200066791-A1

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08-MAR-2000; 2000WO-US005928.

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23306 ACGCGGTTTATCAAAGCTGGATGACGGGCATCAATTATTGGCTGATGCTGAAAGAGGTTA 23365
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The present invention describes the full length genome of Neisseria
meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
represent fragments of the NMB genomic sequence, as the sequence was too
long to go in a record on its own it was split into 8 sequences which
clong to go in a record on its own it was split into 8 sequence by 49980 bp
(i.e. the last 49980 bp of AAF21541 is repeated at the beginning of
(i.e. the last 49980 bp of AAF21507 are repeated at the beginning of
AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
AAF21609, and so on). AAF21545 to AAF21589 to AAF21606 represent pcR
CC AAF21609, and so on). AAF21545 to AAF21589 to AAF2160 represent pcR
CC AAF21609, and so on). AAF2164 is resembled to AAF2160 represent pcR
CC AAF21609, and so on). AAF2164 is resembled to AAF21600 represent pcR
CC AAF21609, and so on). AAF2164 is composition.
CC AAF21609 and so on). AAF2164 is composition of the proteins antibacterial activity, and can
CC AAF21609 and so on on one the ready. Noisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Noisserial bacteria or
CC diagnostic reagent for detecting the presence of Noisserial bacteria or
CC diagnostic reagent for detecting the presence of Noisserial bacteria or
CC diagnostic reading frames (ORFs) or coding sequences within the NMB
CHOOME. The DNA sequences provide further opportunities to find antigenic
CC outer membrane proteins which are more effective in vaccines than the
CC OUT of the proteins which are more effective in vaccines than the
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                                                                                                                                                                                                                                                                                                                                                                                                                             Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence and open reading prevent Neisserial infections.
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Scarselli M,
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11.8%; Score 196.2; DB 3;
Best Local Similarity 51.5%; Pred. No. 7.1e-26;
Matches 532; Conservative 2; Mismatches 481;
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Ratti G,
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frames are used to detect, treat and
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Grandi G;
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28-FEB-2000; 2000GB-00004695
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(GENO-) INST GENOMIC RES.
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Rappuoli R, Frazer CM,
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V, Galeotti
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08-OCT-1999;
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Neisseria meningitidis B nucleotide sequence SEQ ID NO:113

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13-MAR-2001

AAF21612;

AAF21612 XX AAF2 XX AAF2 XX AAF2 XX DT 13-M XX XX

BP.

AAF21612 standard; DNA; 349980

RESULT 7

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949 ATACAACAAAATCCCATGAGCGTTTTATTTCACCTAACACTGTTTATTCTCGATTAAAAT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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                                                                                                                                                                                                                                                                                                                                    New protein from Neisseria gonorrheae, useful for the manufac
medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1467 BP; 356 A; 358 C; 377 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185.8; DB 10; Length
Pred. No. 3.4e-24;
4; Mismatches 487; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 760-761; 815pp; English.
                                                                                                                                                                                                               Masignani V,
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                                                                     12-FEB-2002; 2002WO-IB002069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524; Conservative
                                                                                                                                                                                                               Pizza M,
                                                                                                                                                                                                                                                              2003-058415/05
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Best Local Similarity
                                                                                                                                                                  (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                              WPI; 2003-058415,
P-PSDB; ABP80658
                                                                                                                                                                                                                 Fontana MR,
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                                                          Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
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Pred. No. 3.4e-24;
4; Mismatches 487;
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treatment; Neisseria infection; meningitis; septicaemia; gonorrhea;
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P-PSDB; AAY38653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide specific for pathogenic Neisseria useful in therapeutic or preventative vaccines and for diagnosis.
                                   1486 AAGGGTATTCTTTAAGAGATTCAATGCCTGATAATAAATTACTTCCTGCTTTTAAAAATA
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                                                                                                                                                                                                                                encoding a polypeptide of a Neisseria pathogenic strain
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Matches 524; Conservative
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889 TITCITGGATITITGACTITAITITIAIGCIGIGAIGAIGIAIGITITITGITCGAGCGI
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                                                                                                                                                                         Neisseria meningitidis, Neisseria gonorrhoeae; antigen, vaccine;
treatment, Neisseria infection, meningitis; septicaemia; gonorrhea; ss.
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Pred. No. 1.6e-12;
4; Mismatches 362; Indels
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                                                                                                                                         Neisseria meningitidis strain A complete ORF81 sequence
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27-NOV-1997;
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Pred. No. 5.1e-08;
0; Mismatches 124; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ACF67367 from base 2900001 (Photorhabdus luminescens nucleoti
57 fragments LOCUS ACF67367 Accession Acf67367
                                                                                                                                                                 The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are cources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that the carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and each better the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The carry proteins, vectors containing the genes and Ab are also useful ctherapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens encoded toxins or antibiotics) and as comparating the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. C. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65180 TGGGTGTGGTACTCGCTGCCGGAGGGTATCCTGCTGATTATCACAAAGGGGATATCATTC 65239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65240 ATGGCTTGCCCCAACAAGAAATGAAAGTAGCAAGGTTTTCCATGCTGGTACAGCAATGA 65299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 GTGTATTTGAAGCACAACAAAAAGCGTTAAAATTGGCTGAGCAAATTCAATGGTCTGGGC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 618776 BP; 181854 A; 139249 C; 125634 G; 172037 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 TAGGTATCGTATTGGCTGCAGAGGGATATCCAAAGGATTATCGCAAAGGCGATGAAATCA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65420 GTTTTTACCGCAAGGATATCGGATATCGGGCAATTAACCGATTGAAATAATCATA 65474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAGGCAAGCTAGTCACAAAACGGCGGTCGTGTACTTTGTGTGACTGCGTTAGGCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65300 AAGACAATGATGTTATTACCGCCGGTGGACGCGTTCTGTGTGTTACAGCATTAGGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c sequence of Photorhabdus luminescens and encoded polypeptides e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTTTATCGTCGAGACATTGGTTACAGGCTGTGGAACGAGAACAAGCAAAATA 331
 Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 110000;
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Glaser P, Frangeul L, Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96.6; DB 10; Length
Pred. No. 5.1e-08;
0; Mismatches 124; Indels
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210000
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Begin
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Best Local Similarity 58.0%;
Matches 171; Conservative
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 Taourit S,
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ACF67367 29
Continuation (30 of 57) of WP Sequence split into 57
WP ACF67367 00
WP ACF67367 01
WP ACF67367 01
WP ACF67367 03
WP ACF67367 03
WP ACF67367 03
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/demplification of the genes. Antibodies (Ab) raised against the polymorphisms are used for detection/demtification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful are sensitive to P. luminescens containing the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. Luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                  Antibacterial, fungicide, insecticide, polymorphism, genetic analysis, detection, food, gene expression; plant, animal, microorganism; toxin; antibiotic, biopesticide, virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 95.4; DB 10; Length 1284;
Pred. No. 5.8e-08;
0; Mismatches 116; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1284 BP; 365 A; 263 C; 314 G; 342 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst F,
                                                                                                                                                              Photorhabdus luminescens nucleotide seguence #8385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 8385; 1205pp; French
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                                      ACF69918 standard; DNA; 1284 BP.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                       (first entry)
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Matches 165, Conservative
                                                                                                                                                                                                                                                                  whooping cough; gene; ds.
                                                                                                                                                                                                                                                                                                             Photorhabdus luminescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-148459/14.
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                                                                                                                       20-NOV-2003
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                                                                               ACF69918;
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RESULT 14
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37 TAGGTATCGTATTGGCTGCAGAGGGATATCCAAAGGATTATCGCAAAGGCGATGAAATCA 96

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                                                                                                                                   1115 AAGACAATGATGTTATTACCGCCGGTGGACGCGTTCTGTGTGTTACAGCATTAGGAGAAA 1174
                                                                                                                                                                                                                                                                1175 CCATTATAGATGCACAGAAAATGCTTACCAACAAGAGAAGAGATTGAATGGAATAACT 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as blocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for disgnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                     157 AAGAAGGCAAGCTAGTCACAAACGGCGGTCGTGTACTTTGTGTGACTGCGTTAGGCGAAA
                                                                                                                                                                                                     217 GTGTATTTGAAGCACAACAAAAGCGTTAAAATTGGCTGAGCAAATTCAATGGTCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                    1235 GITITIACCGCAAGGATAICGGATATCGGGCAATTAACCGA 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding Acinetobacter baumannii protein #2917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; plant biocontrol agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-576092/54.
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Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bush D;
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                                                                                                                                                                                                                                                                                                                                         277
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/db xref="GI:48243652"
/trānslation="DPRASLGIVLAAEGYPKDYRKGDEISGLPKSAVKNEKVFLAGVA
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Pred. No. 4.5e-241;
4; Mismatches 4;
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Best Local Similarity 99.2%;
Matches 1597; Conservative 4
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                                                               misc_feature
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complement (1973. .3343)
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/gene="HI0885"
4643. .6382
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                                         Haemophilus influenzae Rd KW20
Bacteria; Proteobacteria; Gammaproteobacteria; Pateurellales;
Bacteria; Froteobacteria; Gammaproteobacteria; Pasteurellales;
Bacteurellaceae; Haemophilus.

1 (bases 1 to 10159)
S. Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,
Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J., Dougherty,B.A.,
Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A.,
Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.I., Glodek,A.,
Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,
Cotton,M.D., Utterback,T., Phillips,C.A., Spriggs,T., Hedblom,E.,
Grotnon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L.,
Geoghagen,N.S., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M.,
Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (15-JUL-1995) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

4 (Bases I to 10159)

Direct Submission

Submitted (17-SEP-1997) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We incorporated their annotation into the /notes fields of the corresponding H. influenzae genes

5 (bases 1 to 10159)

Sis White, O., Clayton, R.A., Kerlavage, A.R., Fleischmann, R.D., Peterson, J., Hickey, R., Karlavage, A.R., Pleischmann, R.D., Direct Submission

Direct Submission
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ATANAEFGNAASVLVGDFIYTRAFQLVAQLESLKILSIMADATNVLAEGEVQQLMNVN
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PID:606125 GB:U00096 percent identity: 64.91; identified
by sequence similarity; putative"
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The whole genome was shifted by 588 nucleotides for a new start
On Sep 30, 1996 this sequence version replaced gi:1221601.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 10159)
White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
Direct Submission
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/db_xref="GI:1573899"
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PRSERFAMLHFCENGGELQTREELLKKWTGRELKPGDRTVDYIRRIRKHFEDHPNTP
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367

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of AR274513 from base 900001 (AR274513 Sequence 1 from patent US
9985 ATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTATCGTCGAGACATTGGTTACAGGGC 10044
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Pred. No. 4.9e-38;
1; Mismatches 57;
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ilarity 85.1%;
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Best Local Similarity
Matches 336; Conserv
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AR274513 00
AR274513 01
AR274513 02
AR274513 04
AR274513 06
AR274513 06
AR274513 06
AR274513 07
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AR274513_13
AR274513_14
AR274513_16
AR274513_16
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AR274513_10
AR274513_11
AR274513_11
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AR274513 09
WPCOMMENT
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formyltransferase (purl)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8780. .10069
| gene="H10888"
| note="similar to SP:P15640 GB:U05126 GB:X51950 PID:147421
| PID:396344 percent identity: 75.18; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9984
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                                                                                                                                                                                                                                                                                                                                                                                                        predicted coding region HI0886"
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                                                                                                                                                                                                                                                                                                'note="hypothetical protein; identified by GeneMark;
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Pred. No. 7.5e-38;
1; Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HI088"
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8780.
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336; Conserv
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COMDIEMENT (1638. . 2348)
Pasteurella multocida subsp. multocida str. Pm70 section 23 of 204 of the complete genome. AE006056 AE004439

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Pasteurella multocida subsp. multocida str. Pm70
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-OCT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
55108, USA
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May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S. and
                                                                                                                                                                                                                                                                                              Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 21145866
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PAT 15-SEP-2000

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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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Bouchardon,A. and Renauld,M.G.
Estent: FR 2785293-A 5 05-MAY-2000;
PASTEUR MERIEUX SERUMS VACC (FR)
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larity 56.1%; Pred. No. 3.3e-37;
Conservative 4; Mismatches 465
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Patent: WO 9924578-A 305 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
PIZZA MARIAGRAZIA (IT); RRANDI GUIDO (IT); MASIGNANI VEGA (IT)
CHIRON SPA (IT); RRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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Pred. No. 3.6e-22;
2; Mismatches 481
                                                                                                                                                                                                                                                                                                                                     DNA
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Sequence 305 from Patent W09924578.
A96272

    1575
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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                                                                                                                       1115 ACAGCGCATTGTT 1127
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                                                                                                                                                                  Gaps
                                                                                                                                                                  18;
                                                                                 Length 1572;
                                                                        Score 197.8; DB 6; Length
Pred. No. 2e-22;
2; Mismatches 480; Indels
                                                                                 11.9%;
51.6%;
                                                                                                                       Best Local Similarity 51.6
Matches 533; Conservative
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ORIGIN
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ë 648

Gaps

169 708 229 768 289 828 349 577

634

517

948

457

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/trānslation="MNQTAINRADVRTRFIFDDMPVRGLHVRLENVWQHIVKQKNYPA
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AEIADDESLGDLLGEGGVYLVLLQPKDGEPWQCVVPLEGGGIAQMLVNYMKRSEQLDT
HIVLSASDBAAGGLLVQRLPEEVLDEBAMEHVSTLARTLTAEELAGLDAQHVLYRLFH
BIPPRVFEPFFFESCTCSRGKVSDMLLMLGGEBEVGGVVVEQGSIEVDCDFCHSKXVF
DETDVNALFGEDVVGVAKGLPRHTVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /traislation="MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREGILRQFAED
BQPVLLPINFAPARRAGRAGNELIGSAMGLINGPALDELTUNRVAPARRAGNADELIGNAMVLIN
BQPVLPVRAPRAPARRAGNADELIGNAMGLLGTAYRYGGTSVGFDCSGEWQUFFKRAM
GINLPRISAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTG
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GWVKTSWLQQLTDALMSNLTLFLVPPCVAVISYLDLIADDWFSILVSASASTLCVLLV
                                                                                                                                                                                                                                 complement (74. .982)
/gene="NMB2000"
/note="conserved hypothetical protein; identified by
Glimmer2; putative"
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/gene="NMB2002"
/note="hypothetical protein; identified by Glimmer2;
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/note="conserved hypothetical protein, identified by
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Glimmer2; putative"
  2000 this sequence version replaced gi:7227263.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       /producE="conserved hypothetical protein"
/protein_id="AAR42327.1"
/db_xref="G1:7227264"
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protein_id="AAF42330.1"
db_xref="GI:7227267"
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producE="conserved hypothetical protein"
/protein_id="AAF42338.1"
/db_xref="GI:7227265"
                                                                               MC58"
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                                                                            meningitidis
                                                                                                                                                         /db_xref="taxon:122586"
                                                       1. .15053
/organism="Neisseria me
/mol_type="genomic DNA"
/strain="MC58"
                                                                                                                                                                                 /note="serogroup: B"
complement (74. .982)
/gene="NMB2000"
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                                                                                                                                                                                                                                                                                                                                                                                     table=11
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/transl_table=11
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/gene="NMB2001"
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/gene="NMB2003"
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/gene="NMB2003"
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/transl_table=
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                             FEATURES
     COMMENT
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Neisseria meningitidis MC58

Neisseria: Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae, Neisseria.

1 (bases 1 to 15053)

2 Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.J., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D.,
Hickey,B.A., Mason,T., Ciacko,A., Parksey,D.S., Blair,E.,
Cittone,H., Clark,B.B., Cotton,M.D., Utterback,T.R., Khouri,H.,
Qin,H., Vamathevan,J.G., Gill,J., Scarlato,V., Masignan,V.,
Pizza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R.,
Rappuoli,R. and Venter,J.C.
                                                                                                       1305
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  GTTACGGGAGAAAAACATCTCCTTTTTAGATAG---CTTAAAATATAAATCAGGAGCTC 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAATTTAGATAATGGTTATCATTTTGTTGTTTTACATCATAGAGGGAGTCATATTCCCT 1605
                                                                                                                                                                                                                                                                                                           1366 ATTTAGCGAAAGAGCAAGGCTTTCAGACATATTTTTATTCAGCTCAAGCTAGGGATGATA 1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    995 TTGGCTACGGCACGGCGACAATATGCCCGATGAGAAGCTGCTGCTGCCGTTGTTCGACAAAA 1054
                                                                                                                                         815 ATGCGATACCGCACGCCAACGGCTTGGAACAAATCAGCGGCGGTAACCAATATGTTCC 874
                                                                                                                                                                                                                                                                                                                                           875 GCCTCGCCAAAGAGCAGGGCTATGAAACGTATTTTTACAGCGGCAGGCGGAAAACGAGA 934
                                                  695 GCTACGGACGCGAAACTTCGCCGTTTTTAACCCGGCTGTCGCAAGCCGATTTTAAGCCGA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                               935 TGGCGATTTTGAACTTAATCGGTAAGAAATGGATAGACCATCTGATTCAGCCGACGCAAC 994
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Direct Submission
Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                    TIGITGGTAAAACTTATTCAGGAGGAAAGCTAACAGCAATTTCTTTACCAATGTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genome sequence of Neisseria meningitidis serogroup
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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10659 GCTACGGACGCGAAACTTCGCCGTTTTTAACCCGGCTGTCGCAAGCCGATTTTAAGCCGA 10718
NSYTHLIANDFDWILQYLFAQQNNIAVANNQKLARNEKVTNSKTKLDILQEAWETLLPH
RKLHITADDIQYSAVDNEBLYSASNMSDGERALFYILGGQVLSYDDGSVLIFDEPELHI
HKSIISNLWDKIEELRPDCSFLJITHDIEFAATRVAKKYVIRNYYPTPAWDISEVERI
NPDEETITHIGSRRFDILFYDGNNNSLDIATRRYCYPDWTIIPRGACKOVIQSVSEK
KLSNEMPLLANLKCSGIVDLDSRDERBIEQLANLGIYILPVSEIENLFSLTDVAKEILK
TOYSDEELLANLANGFKSELIKYIDNEKDDVLLDEFVVXQVRRKIDNYLKNIDLSSKI
TSTDWKKSLLANEINGFKSELIKYIDNIKDDVLLDEFVVXQVRRKIDNYLKNIDLSSKI
TSTDWKKSLLANEINGFKSELIKYIDNIKDGVGARGA
                                                                                                                                                                                                                                                                   /Jote="This region contains a gene with one or more premature stops or frameshifts, and is not the result sequencing artifact; similar to SP:009530 PID:733602 percent identity: 61.70; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10422 CGTTCGACACGAAACAAGAGCACGGTATTTCGCCCAAACCGACATACAGCGCATCAAAG
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Pred. No. 2.4e-22;
2; Mismatches 481;
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ilarity 51.5%;
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Best Local Similarity
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STVGAVFTTNRFCAAPVHIAKSHLFDBDGYRALVINTGNANAGTGAQGRIDALAVCAA
STVGAVFTTNRFCAAPVHIAKSHLFDBDGYRALVINTGNANAGTGAQGRIDALAVCAA
SRAQIGCKROVLPFSTVGUILBPLPARKIIAAFRGAPARAGATTDTVPKAA
SREGKVGKPHTVRATGIAKGSGNIHPNMATHLGFIATDAKVSGPVLQLMTQBIADETF
NTITVDGDTSTNDSFVIIATGKNSQSIDNIADPRYAQLKELLCSLALELAQAIVRDG
EGATKFTYNVENAKTRDEARQAAYAVRRSPLVKTAFFASDPNLGRLLAAIGYAGVAD
LDTDLVFWTLDDILVBHGGRAASYTEAQGAVMSKABITVRIKLHRGQAAATVYTCD
LSHGYVSINADYRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTSTFPRRLARKIRQTRRLSRKSIAFLFLLAGSALVALTALFFA
HLADPALELNKLVQQYPWFAWVALPLGLPLIAWLTRKFAPFTAGSGIPQVIASILSLP
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PKGMOBNDLMAGAAGGLAGTRIPTELGKGIMLRWERQILLGVLASGFI
QVAIQGNNPYPSGFNGGYLEH FNAPALSGLVCGAAGGLFGRLLYRGAAAFAPRKIG
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TYLKILGIDTAVYHNAAQFIDFWLKPNVVLLAPLYQURKRIFNVMLPYIVSQLAGS
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SAVVVMEMTGGQSLLFWMLIACI FASQVSRQFSPRPFYHASGMRFRQRVLQETAAQTG
                                                                                                                                                                                                                                                                                                                                                                                                          PID:150243
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YIEEQLKEKAHRISAHRALKLNPNVNKIPEKSAKTYLSYGQNWDGIDVSNRKNYRWDN
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of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ABC transporter, ATP-binding protein-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to PID:862629 percent identity: 53.03; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="glutamate N-acetyltransferase/amino-acid
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:M65216 SP:P38434 GB:S85363
PID:246444 percent identity: 98.77; identified b
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                                                                                  hypothetical protein"
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/producC="chloride channel
/protein_id="AAF42333.1"
/db_xref="G1:7227270"
                                                                             /product="conserved hypo
/protein_id="AAF42331.1"
/db_xref="G1:7227268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF42332.1"
/db_xref="GI:7227269"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity; putative"
/codon_start=1
/transl_table=11
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     putative"
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/gene="NMB2005"
/note="similar to
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/gene="NMB2006"
4747. .6156
/gene="NMB2006"
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7881. .9524
/gene="NMB2008"
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/gene="NMB2005"
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/gene="NMB2007"
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/gene="NMB2008"
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/transl_table=:
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Pizza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
Scarlato,V., Rappuoli,R., Frazer,C.M. and Grandi,G.
Neisseria genomic sequences and methods of their use
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Neisseria meningitidis
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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Sequence 113 from Patent W00066791.
AX044034 GI:11342918
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Patent: WO 9924578-A 309 20-MXY-1999;
PIZZA MARAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
Location/Qualifiers
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Pred. No. 1.7e-20;
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                 18;
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 Patent: WO 0066791-A 113 09-NOV-2000;
CHIRON CORPORATION (US); THE INSTITUTE FOR
Location/Qualifiers
                                                                                                                                                                                                                                                             tch 11.8%; al Similarity 51.5%; 532; Conservative ::
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/tranalation="MKKSTPULEVSSLLTASEIAYREVFGIETLPAAKMAETFALTF
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MGESESAAHIKLFGYGRETSPFLTKLSQADFKPIVKQSYSAGFMTAVSLPSFFNIVIPI
ANGLEQISGOTNWHFLAKEQOYETYFYSAQAENQMAILALIGKKMIDHLIQPTQLGY
GNGDNWPDEKLLPLFDKINLQQGRHFIYLHGRGSHAPYGALLQPQDKYFGENDIYDKY
DIYNIHKTDGANGTYFFGLAFQQSTRFIYLHGRGSHAPYGALLQPDQNAVQPDSYIVPLV
LYSPDKAVQQAANQAFGETAFFQQCSTFITHILGYDMPVSGCREGSVTGNLITGDA
GSLNIRNGKAEYVYPQ"
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                                                      CCAATTATTTATCGTTGGGTTATTTTATAGGACGAATTGTTCCTTATGAGATATTTTCTT
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Nassif,X., Tinsley,C., Aujame,L., Perrin,A., Rokbi,B.
Bouchardon,A. and Renauld,M.G.
Patent: FR 278523-A 56 05-MAY-2000;
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CKPFLREDSRICMATKGLEBETGRLLKDVAYDITGENYSLAVLSGPTPAKELAMGLPT
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                           CDS
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20295086
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1426 TGCATATGATCAATTTTTTAGGAGGAGCTTGGATTGATGATATTTCGTTTTCCAGATAATG 1485
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1. .288108
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                                                      994
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Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.
Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.
Bibmission
Submission
Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara,
Kanagawa 228-8555, Japan
(E-mail:hattori@genome.ls.kitasato-u.ac.jp,
URL:http://genome.ls.kitasato-u.ac.jp/, Tel:81-42-778-8194,
                                                                                                             1486 AAGGGTATTCTTTAAGAGATTCAATGCCTGATAATAAATTACTTCCTGCTTTTAAAAATA
                                                   935 regeratrricaacriraareegraagaaaregaraegeereereereereegeeae
                                                                                                                                                                                                                                   1546 TTAATTTAGATAATGGTTATCATTTTGTTGTTTTACATCATAGAGGGAGTCATATTCCCT
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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/mol_type="genomic DNA"
/strain="03:K6"
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AP005083.1 GI:28807856
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/codon_start=1
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                                                                                                                                                                                   VQAGDELTVLDI SMEKNWAGLEQALAQGAHVEYADHHKAGDÎ PQHGNLDAHIDLDANM
CTALIYDKLLEGRFHWAITAAYGDNI.IAKADVLADQAGLNNEQKAQIKELGTLINYN
GYGSKVDDLHFHPADLYRALAVQYI SPEVIEDKASTTYQLQGAYQQDMDAAQAVPATH
ESDTLKLFELPNTAASRRISGYYGNMLANQNEDSAHAVLTENADGTYTVSLRAPLANK
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YSGFAFLGCFCVWRWRQRWAVAMGIILFSAVIEWLQGYVGRQTSWLDLVANSTGILTG
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IDYHLISALEAGLPDCAGVALGIDRLIMLALGCDHIDQVTAFPFPIA"
                                                                                                                                                                  translation="MNYDIFNGDADGIIALLQLRLADPIDSQLITGVKRDIKLVEKVD"
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GB:AAF93507.1 (AE004122) percent
                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:AAF93506.1 (AE004122) percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="transcriptional reguator, TetR family"
/protein id="BAC61099.1"
/db_xref="GI:28807862"
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/protein_id="BAC61101.1"
/db_xref="G1:28807864"
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                                                                                                                                                                                                                                                                                                                           complement (5042. .5677)
/gene="VP2836"
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/gene="VP2837"
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/note="similar to GB:AJ
identity 56 in 318 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITITICITAGCGGGTGTCGCAGAACAAGAAGCCAAGCTAGTCACAAACGGCGGTCGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 CTTTGTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAAAAAAGCGTTAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 GCTGAGCAAATTCAATGGTCTGGGCGTTTTTTATCGTCGAGACATTGGTTACAGGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GAACGAGAACAAGCAAAATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAAATATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus ducreyi 35000HP
Haemophilus ducreyi 35000HP
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.

1 (bases 1 to 300521)
Munson, R.S. Jr., Ray, W.C., Mahairas, G., Sabo, P., Mungur, R.,
Johnson, L., Nguyen, D., Wang, J., Forst, C. and Hood, L.
The Complete Genome Sequence of Haemophilus ducreyi
Unpublished
Length 288108;
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Best Local Similarity 61.0%; Pred. No. 1.4e-12;
Matches 233; Conservative 1; Mismatches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      authentic frameshift.
This region contains an authentic frameshift or in-frame stop in the coding sequence and is not the result of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1069 TATCTAATATCCTCTTTATCATAAATCTAAGCCTATGAAATCGGGCTCTCCGVAAAATT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTACGGGAGAAAAACATCTCCTTTTTT---AGATAGCTTAAAATATAAATCAGGAGCTC 1245
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Neisseria meningitidis serogroup A strain Z2491 complete genome;
segment 2/7.
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1 (Dases 1 to 349061)

Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Morelli,G., Bacham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Cuall,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491

Nature 404 (6777), 502-506 (2000)
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                                                                                                                                                                                                              230 ACGCGGTTTATCAAAGCTGGATAACGGGCATTAATTATTGGCTGATGCTGAAAGAGATTA
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                                                                                                                                                                                                                                                                                                                                     350 GCGTGTTGGAAGTCATGTTGTTTTTGCAGCCTTGCCAAGTTCCGCCGTAAGACGCAT----
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                                  TTACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTTGTTAATAATGTACATT
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Neisseria meningitidis 22491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                                                                                                                                                                                                                                                                  /translation="Maiqnkkiajtdvvlkdahqslfatrlrlddmlpiateldkvgy
WSLETWGGATFDSCIRFLGEDPWVRLRELKKAIPNTPLQMLLRCQNLLGYRHYADDVV
DRFVDRCIANGMDIFRIFDALNDPRNMQAALQAVKKHGGHAQGTLSYTTSPVHTLQTW
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LLKAIEAGIDGIDTSISSMSGTYGHPATESMVATLQGTAYDTGLNIHQLEKIAAYFRQ
VRKKYAKFEGQLRGIDSRILVAQVPGGMLTNIESQLKQQNATDKLDLVLQEIPKVRED
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Patent: WO 9924578-A 307 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT); CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGTCGTGTACTTTGTG 198
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protein_id="AAP95686.1"
'db_xref="GI:33148166"
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Pred. No. 5.6e-10;
4; Mismatches 362; Indels
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Pred. No. 1.6e-10;
0; Mismatches 89
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Sequence 307 from Patent WO9924578.
A96274.
A96274.1 GI:6780029
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
complement (8397. .10202)
                                                           /locus_tag="HD0783"
complement(8397. .10202)
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codon_start=1
transl_table=11
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ilarity 67.1%;
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9967. 3191
/gene="81yX"
2967. 3191
/gene="81yX"
/gene="81yX"
/gene="81yX"
/note="NMA0371, 81yX, SLYX protein homolog, len: 74 aa; pinlar to SLYX HARIN P44795 SLYX protein homolog (73 aa), fasta scores; E(): 0.0017, 33.8% identity in 74 aa overlap, and SLYX ECOLI P30857 SLYX protein (72 aa), fasta scores; E(): 0.24, 32.4% identity in 68 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jours - NAMANATA, thif, probable Thir protein, len: 256 aa; similar to e.g. THIF ECOLI PROMAB THIR protein (251 aa), sata scores; E(): 0, 43.1% identity in 246 aa overlap, and WORB ECOLI PRIZAR molybdopterin biosynthesis MORB protein. (249 aa), fasta scores; E(): 0, 43.9% identity in 244 aa overlap (note that N.m. does not have orthologs of any other molybdopterin biosynthesis proteins). Contains Pfam match to entry PF00899 Thir_family, Thir family.
                                               /gene="NMA0370"
1578. .2966
1578. .2966
/note="NMA0370"
/note="NMA0370, probable integral membrane protein, len:
/note="NMA0370, probable integral membrane protein, len:
462 aa; similar to hypothetical proteins e.g. Y325_HAEIN
P44640 hypothetical protein H10325 (450 aa), fasta scores;
P5: 0, 49.8% identity in 464 aa overlap"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                            /tränslation="mmavvvvavivmluslsrvhvvlslfigafvggavagmplqnia
padgovsgagiipvprkglibesgakilabfyamlgastamlitslipQuadvyrkliktinr
ggmplsyrsgegovyrklilsiiluwgamsquiipiiHnafipmivppliluvFnblkiib
RLiacvitfglvttymflpygggaiFlnbillglilgniisaapQldvkninvmaamaiPal
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KYEDSLVLGAALGFAVFRMLGVINRDKANDVFGEIKMAMVGFIMLAAGGRAAWNA
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GFSPLATVAIVGTAGALGDAGSPASDSTLGFTMGLNADGQHDHIRDSVIPTFIHYNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="TrEMBL:Q9JWH4"
/translation="WDAVQEFEHRITELEIQSALQEDVIAGLNAMVAELRQTLDLQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFGRLSPLGSDGPPLAVYEYPVGFICLQGKTAYFRSGGKRFHRI
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                                                                                                                                                                                                                                                                                       /product="putative integral membrane protein"
/protein id="CAB83671.1"
/db_xref="G1.7379123"
/db_xref="GOA:Q9JWH5"
/db_xref="TrEMBL:Q9JWH5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'transI_table=11
product="very hypothetical protein NMA0372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3562. .3571
/note="Core DNA uptake sequence: gccgtctgaa"
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/product="SLYX protein homolog"
/protein_id="CAB83672.1"
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/db_xref="GI:7379125"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3271. .3423)
/gene="NMA0372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3271. .3423)
/gene="NMA0372"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ThiF protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table=11
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/transl_table=:
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/transl_table=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="NMA0369, hemK, HemK protein, len: 273 aa; similar co e.g. HEWK ECOLI P371 a8, fasta scores; E(): 0, 42.3% identity in 279 aa overlap. Contains PS00092 N-6 Adenine-specific DNA methylases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="trembl:09JWH6"
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RQRADRLAQRRLAQREVAYILGAREFYGRRFTVNPSVL:PRPETEHLVEAVLARLPEN
GRVWDLGTGSGANGEPVAYILGRPDAFVRANDISPPALETARKNAADLGARVEFAVGSWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānglation="MOEQNRKSSFPIVMLLVSVALWIASLSNVAFYLGNHGSMEGLTV
LILGSIFASLDIRYCAVYANYVWLAAIVLLALRKKVVPVHAAFWGLALVAFSVKAVYV
DEAGNTSDIVRYGAGFYLWYAAFAVASIGTFAGKNKERKAASAADGTKODV"
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DRLAEGGFLLLEHGFDQGAAVRGVLAENGFSGVETLPDLAGLDRVTLGKYMKHLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="serogroup: A"
complement(24. .206)
/note="ATR repeat; hmmfs hit to HMM ATR (1 - 183), score:
310.39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="NWA0368, probable integral membrane protein, len:
153 aa; contains four probable transmembrane domains"
                                                                                                                                                                                                                  Sanger Centre are
                Parkhill, J.

Submitted Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (30-Mak-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

Notes:

Details of N. meningitidis sequencing at the Sanger Centre aravailable on the World Wide

available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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/protein_id="CABB3669.1"
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/note="Core DNA uptake sequence: gccgtctgaa"
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/gene="hemk"
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|abel=DUS
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                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:122587"
                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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/gene="NMA0368"
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671. .1492
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/gene="hemK"
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'gene="hemK"
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/transl_
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4471. .7224
/gene="ppc"
4471. .7224
/gene="ppc"
4471. .7224
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/EC number="4.1.1.31"
/note="NMAD174, ppc, phosphoenolpyruvate carboxylase, len:
917 aa, simlar to many e.g. CAPP RHOPA 032483
phosphoenolpyruvate carboxylase (EC 4.1.1.31) (936 aa),
fasta scores; E(1:0, 43.3* identity in 928 aa overlap.
Contains 2x Pfam match to entry PF00311 PEPCase,
Phosphoenolpyruvate carboxylase, PS00017 ATP/GTP-binding
site motif A (P-loop), and PS00393 Phosphoenolpyruvate
carboxylase active site 2"
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FEGQLAVYRPDLPDSPCYACLFDGGSAADGICSLFGVFSPLVGIIGSTQAAEALKILL
DAGEESHGRLAVYRALEGGWQYFDLFRNFECFVCGAER"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAAAGTTATTTGTCTGTTTGTTTGTTTGTTTGTTTTGTTTTTTCAAAATATAGAA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649 TIACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTTAATAATGTACATT
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                                                                                                                                                                                                                                                            complement (1847. .4257)
/gene="thif"
/note="Pfam atch to entry PF00899 Thir_family, Thir family, Boore 186.60, E-value 4.1e-52"
complement (4418. .4427)
/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
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65325 CGTTCGACACGAAACAAGAACACGGTATTTCGCCCAAAACCGACATACAGCCGCCATCAAAG 65266

CCAATTATTTATCGTTGGGTTATTTTATAGGACGAATTGTTCCTTATGAGATATTTTCTT 1068

55265 ccaattattaccricccriatititarccaacccrataccaiatcarriagir

TATCTAATATTCCTCTTTATCATAAATCTAAGCCTATGAAATCGGGCTCTCCGVAAAAT 1128

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65145 AAAATATCGTCCTGA---TTATGGGCGAAAGCGAAAGCGCGGCGCATTTGAATTGTTTG 65089
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MARGAATATAATTTAATTAATGGGGGAAAGTGCGACCTCAAGTCATTTTAGTGCTTTTTG
                                                                           GTTACGGGAGAAAAACATCTCCTTTTTT---AGATAGCTTAAAATATAAATCAGGAGCTC
                                                                                                               65088 GCTACGGGGGAAACTTCGCCGTTTTTGACCCAGCTTTCGCAAGCCGATTTTAAGCCGA
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                                                                                                                                                      TIGITGGTAAAACTTATTCAGGAGGAAAGCTAACAGCAATTTCTTTACCAATGTTTTTTA
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Search completed: December 23, 2004, 18:16:17 Job time : 7041 secs

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8 ATCACAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGGGATATCC
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Sequence 10413, A
Sequence 10306, A
Sequence 10749, A
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Sequence 1, Appli
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                                                           December 23, 2004, 15:49:34; Search time 151 Seconds (without alignments) 7795.142 Million cell updates/sec
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US-09-328-352-2917
US-09-252-991A-10413
US-09-252-991A-10306
US-09-263-681A-3189
US-10-204-708-2
US-10-204-708-3
US-10-204-708-3
US-10-204-708-3
US-09-489-039A-1
US-09-489-039A-1
US-09-806-7088-80
US-10-204-708-80
US-10-204-708-3
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US-09-643-990A-1
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                          824507 seqs, 355394441 residues
         version -
                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
                                                                                                                               IDENTITY NUC
Gapop 10.0 , Gapext 1.0
         GenCore (c) 1993
                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                              US-10-698-235-1
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17.7 1830121
5.8 1335
5.3 1347
6.3 1383
6.3 1410
4.4 10467
4.3 19513
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4.0 1055
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6669
6583
11049
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                                                                                              Title:
Perfect score:
                                                                                                                                Scoring table:
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292.4
292.4
95.4
88.2
88.2
88.2
88.2
74
73.6
73.6
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                                                            Run on:
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13, Appl
2, Appl
10, Appl
10, Appl
30, Appl
63, Appl
63, Appl
63, Appl
63, Appl
63, Appl
63, Appl
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.'
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.7%; Score 292.4; DB 4; Length 1830121; Best Local Similarity 85.1%; Pred. No. 8e-54; Matches 336; Conservative 1; Mismatches 57; Indels 1; G
                                                Sequence
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                           US-10-204-708-21
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US-10-204-708-23
US-10-204-708-13
US-10-204-708-19
US-10-204-708-10
US-10-204-708-69
US-10-204-708-69
US-10-204-708-9
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ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: CUNKNOWN:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Michelle S. Marke
REGISTRATION NUMBER: 41, 971
REFRENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELERAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Sequence 1, Application US/10329960

### Sequence 1, Application US/10329960

### Patent No. 6742201

### TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragm

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: Thereof, and Uses Thereof

### TITLE OF INVENTION: UNBER: US 09/643,990

### PRIOR PEPLICATION NUMBER: US 09/643,990

### PRIOR PEPLICATION NUMBER: US 08/487,429

### PRIOR APPLICATION NUMBER: US 08/426,787

### PRIOR PELING DATE: 1995-04-21

### NUMBER OF SEQ ID NOS: 1

### SEQ ID NO 1

### IEBNGTH: 1830121
                                                                                                                                                                                                                                                                                               941919 ATATCACAATGGGATCTGCGAGCTTCT-TTAGGTATCGTATTGGCTGCAGAGGGATACCC 941977
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                                                                                                                                                                                                                                                               8 ATCACAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGGGATATCC
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                                                                                                                                                             Length 1830121;
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Pred. No. 8e-54;
1; Mismatches 57;
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  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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NAME/KEY: misc_feature
NCGATION: (9921)
OTHER INFORMATION: n equals a, t,
FEATURE:
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                                                                                                                                                     Query Match
Best Local Similarity 85.1%;
Matches 336; Conservative
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LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
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US-09-643-990A-1
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941978 AAAAGATTATCGCAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 942037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGAACGAGAACAAGAAATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAAT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamilton O. Smith
J. Craig Venter
J. Craig Venter
INVENTION: The Nucleotide sequence of
Thereof, and Uses Thereof
Thereof, and Uses Thereof
                                                                                                                                                                                   GAAAGTTTTCTTAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGTCG
                                                                                                                                                                                                                                                                                       TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAAAAAAGCGTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVER
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 90,302
REGISTRATION NUMBER: 90,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1830121 base pairs
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TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MD
COUNTRY: USA
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US-09-643-990A-1
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NAME/KEY: misc feature LOCATION: (145058)..(145058) OTHER INFORMATION: n equals a, t, g or c OTHER INFORMATION: n equals a, t, g or c g or c g or FEATURE:
NAME/KEY: misc\_feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a, t, g or g or g or g or ö or or ຫ FEATURE:
NAME/KEY: misc\_feature
LOCATION: (117136)...(117136)
OTHER INFORMATION: n equals a, t, g
FEATURE:
NAME/KEY: misc\_feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g מ D b ρ NAME/KEY: misc\_feature LOCATION: (131350). (131360) OTHER INFORMATION: n equals a, t, g FEATURE: NAME/KEY: misc\_feature LOCATION: (133910). (139910) OTHER INFORMATION: n equals a, t, g מ ρ NAME/KEY: misc feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals a, t, FEATURE: NAME/KEY: misc feature LOCATION: (122167)..(122167) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a, t, LOCATION: (140398)..(140398) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc\_feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (102696)..(102696) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEX: misc\_feature
LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc\_feature
LOCATION: (140398)..(1/

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1098 CTCAGGTATCGGTCAATCACCAGAAGATACTAAAATCTTCCATGCAGGCACTGCTACTCG 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1079 TGGGCGTGGTACTGGCCGGCGGCGACTACCGGGCGACTACGCCAAAGGGCGAGGCCAACGGTCATCG 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1259 GCGTGTCCGCCGCCCAGCAACAGGCCTATCGCCTGGCCGAGAAGATCCGCTGGAACGCT 1318
                                                                                                                                                      95 CAGCGGATTGCCTAAAAGTGCGGTCAAAAACGAGAAAGTTTTCTTAGCGGGTGTCGCAGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 GCGGATTGCCTAAAAGTGCGGTCAAAAACGAGAAAGTTTTCTTAGCGGGTGTCGCAGAAC 156
                                                                                                                                                                                                                                                                                                                                                                                                         1278 TATGCAATACCGCAGTGACATTGGTTACCGTGCTATTGCTCGTGAAAAAGCTGAATA 1334
                                                                                                                                                                                                                                                                                                                                                                                  275 GCGTTTTTATCGTCGAGACATTGGTTACAGGGCTGTGGAACGAGAACAAGCAAAATA 331
                                                                                                                                                                                                                                                                                                       215 AAGTGTATTTGAAGCACAACAAAAAGCGTTAAAATTGGCTGAGCAAATTCAATGGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1199 AGGATGGCCAGGAGGTCACCTCCGGCGGCGGGGTGCTCTGTGCCACCGCCATCGGCGAGA
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                                                                              35 ATTAGGTATCGTATTGGCTGCAGAGGGTATCCAAAGGATTATCGCAAAGGCGATGAAAT
                                                                                                                   155 ACAAGAAGGCAAGCTAGTCACAAAAGGGGGGTCGTGTACTTTGTGTGACTGCGTTAGGCGA
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     Length 1335
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Pred. No. 3.2e-10;
0; Mismatches 123; Indels
 Score 95.4; DB 4; Dred. No. 8.6e-12; 0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
 Query Match
Best Local Similarity 57.6%;
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%;
Best Local Similarity 56.8%;
Matches 162; Conservative
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| Patent No. 6562958
| Patent No. 6562958
| GENERAL INFORMATION: ULLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION UNMBER: US/09/328,352
| CURRENT FILING DATE: 1999-06-04
| CURRENT FILING DATE: 1999-06-04
| SEQ ID NO 2917
| LENGTH: 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941919 ATATCACAATGGGATCTGCGAGCTTCT-TTAGGTATCGTATTGGCTGCAGAGGGATACCC 941977
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17.7%; Score 292.4; DB 4; Length 1830121;
Best Local Similarity 85.1%; Pred. No. 8e-54;
Matches 336; Conservative 1; Mismatches 57; Indels 1; G
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NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a, t,
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7 ORGANISM: Acinetobacter baumannii
US-09-328-352-2917
NAME/KEY: misc feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a,
                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (147197)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
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US-09-328-352-2917
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NAME/KEY: promoter DOME/LIA1)
LOCATION: (1)..(1141)
LOCATION: Consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
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                                                                                                                                               97 GCGGATTGCCTAAAAGTGCGGTCAAAAACGAGAAAGTTTTCTTAGCGGGTGTCGCAGAAC 156
                                                                                                                                                                                                              305 AAGGCCTGGCCGAGGCCGCCGCGCTGGACGGCAAGGTGTTCCACGCCGGCACCGCGCTGA 246
                                                                                                                                                                                                                                                                                                                                                       245 AGGATGGCCAGGAGGTCACCTCCGGCGGCGGCGTGCTCTGTGCCACCGCCATCGGCGAGA 186
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                                                                         365 TGGGCGTGGTACTGGCCGCCGCCGTATCCGGGCGACTACGCCAAGGCGAGGTCATCG 306
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Patent No. 6794342

GENERAL INFORMATION:
PAPPLICATY: The University of British Columbia
TITLE OF INTERPLEMENT REGULATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03

PRIOR PILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

LENGTH 1141
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ORGANISM: Artificial sequence
FEATURE:
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Patent No. 6551795
GENERAL INFORMATION:
PAPLICATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
PRICE REPRENCE:
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PRICE REPRENCE:
PRICE REPRENCE:
PRICE APPLICATION NUMBER: US/09/252,991A
CURRENT PAPLICATION NUMBER: US 60/074,788
PRICE REPRENCE:
PRICE REPRENCE:
PRICE PLING DATE: 1998-02-18
PRICE PLING DATE: 1998-02-18
PRICE PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10749
                                    Sequence 10366, Application US/09252991A

Factor 2016, Application US/09252991A

Factor 1006, Application US/09252991A

Factor 1006, 651795

GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196, 138

CURRENT APPLICATION NUMBER: US 60/074, 788

FRIOR APPLICATION NUMBER: US 60/094, 190

FRIOR APPLICATION NUMBER: US 60/094, 190

FRIOR FILING DATE: 1998-02-18

FRIOR PRINT DATE: 1998-07-27

SEQ ID NO 10306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          957 TGGGCGTGGTACTGGCCGCCGGCGGCTATCCGGGCGACTACGCCAAGGCGCGAGGTCATCG 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 TAGGTATCGTATTGGCTGCAGAGGATATCCAAAGGATTATCGCAAAGGCGATGAAATCA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAAGGCAAGCTAGTCACAAACGGCGGTCGTGTACTTTGTGTGACTGCGTTAGGCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 88.2; DB 4; Length 1 Pred. No. 3.2e-10; 0; Mismatches 123; Indels
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Pred. No. 3.2e-10;
0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.3%;
Best Local Similarity 56.8%;
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.3%;
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Best Local Similarity 56.8
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-252-991A-10749/C
RESULT 6
US-09-252-991A-10306
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JUNEARAL INFORMATION:

APPLICANT: DIEFENBROCK, Christian
APPLICANT: BIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: DASSESSING DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FAPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
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PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                   .088 caacagcraaggrarincaagcaggaacaaarraacggcrcaaggrgaagragracag 1147
                                                                                                                                                                                                                                                                                    1148 caggaggccgagrarrargrgcaacrgcrrraggggaagararcgaacaagcrcaaaaa 1207
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61 GATATCCAAAGGATTATCGCAAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCA 120
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                                                                                                             121 AAAACGAGAAAGTTTTCTTAGCGGGTGTCGCAGAACAAG---AAGGCAAGCTAGTCACAA
                                                                                                                                                                                                                              178 ACGGCGGTCGTGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAACAAA
                                                                                                                                                                                                                                                                                                                                            AAGCGTTAAAATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTTATCGTCGAGACATTG
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Patent No. 6677731
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ORGANISM: Artificial Sequence
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON:
TITLE OF INVENTION:
TITLE OF INVENTION:
DIAGNOSTICS AND THERABEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION WUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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                                      768 TTDKRNNGAYTKYTTTNNNNTYRGVVTNTAARDGWANNNNNNNNNNNNNNNNNNNNNNGWSDMVTWW 827
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  TACCAATCTTGGATTGGACCTGTTAATTACTCACTTGCATTTAAAGAAATTAATGAGATA 776
                                                                                                                   777 ACAAAIGCTGGCTIAACAAIGAIAGAIAAAITCAIAIATACCAIIGTIAITIGGIITAITI 836
                                                                                                                                                                                                                                    897 ATTITIGACTITATITITATGCTGTGATGTATGTTTTTTTTTCGAGCGTATACAACA 956
                                                                                                                                                 1 AAGTAATATCACAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGG
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SEQ ID NO 3189
LENGTH: 1299
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APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BIEFENBROCK, Christian
APPLICANT: BIEFELIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Dy Assessing DNA Methylation
ITILE OF INVENTION: Dy Assessing DNA Methylation
ITILE OF INVENTION: DY ASSESSING DNA METHYLATION
INVERING APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
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                                                                                                                                                                                                                       3938 AAATATTATTGAATTATATATATTTTAAATGGGTGAATTGTATAGTATGTGAATTATAGT
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; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-39
                                                                                                                                  10;
                                                                                       Length 19513;
                                                                                                                                  Indels
                                                                                    Score 71.6; DB 4; I Pred. No. 2.6e-06; 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-204-708-74
; Sequence 74, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
                                                                                    Query Match
Best Local Similarity 47.4%;
Matches 287; Conservative
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APPLICANT: DIEK, Alexander
APPLICANT: DIEK, Alexander
APPLICANT: DIEK, Alexander
APPLICANT: DIERENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
FILE REFERENCE: 2001.04-06
FRICH APPLICATION NUMBER: DE 10019058.8
FRICH APPLICATION NUMBER: DE 10019058.8
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FRICH APPLICATION NUMBER: DE 10019058.8
FRICH FILING DATE: 2000-04-07
FRICH APPLICATION NUMBER: DE 10019058.8
FRICH APPLICATION NUMBER: DE 10043826.1
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  Sequence 39, Application US/10204708 Patent No. 6677731
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS 45
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                                                                                                                                                                           Score 69.4; DB 2;
Pred. No. 7.8e-06;
TITLE OF INVENTATION 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Be
STREET: 620 Newport Center Drive 16
CITY: Newport Beach
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 289; Conservative
                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                  ZIP: 92660
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                                                                                                                                                                                                   Gaps
                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-74
                                                                                                                                                                    Score 70; DB 4; Length 5152;
Pred. No. 4.1e-06;
0; Mismatches 315; Indels
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Patent No. 5993877
GENERAL INFORMATION:
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David S.
APPLICANT: Willer, Louis H.
APPLICANT: Wellems, Xin-Labaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
WINBER OF SEQ ID NOS: 98
LENGTH: 5152
                                                                                                                                                                    Query Match
Best Local Similarity 47.0%;
Matches 283; Conservative
                                                                                                ORGANISM: Artificial Sequence
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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE: NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67.6; DB 4; Length 8961;
Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches 437;
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-1
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 80
LENGTH: 8961
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (5096)
OTHER INFORMATION: n is a or g or c or
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gary Breton et. al TITLE OF INVENTION: WICLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: WICLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS CURRENT FILE STORY OF SECONDAL OF SECONDAL STORY APPLICATION NUMBER: US/09/489,039A PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR APPLICATION NUMBER: US 60/117,747
       619
                                                                               883 ATAAACTTICTIGGATTITIGACTTIATTITITATGCTGTGATGATGTATGTTTTTGTTC 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DA Assessing DNA Methylation
FILE REPERENCE: 5013.101.
FULLS REPERENCE: 2013.101.
FULLS APPLICATION NUMBER: PCT/F901/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                           15385 AAACACATACAAGTACATCCATATATATATATCCTTAACCCACAATACATATAC 15331
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4.1%; Score 67.8; DB 4; Length 741;
Best Local Similarity 54.2%; Pred. No. 7.4e-06;
Matches 160; Conservative 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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US-09-489-039A-1
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US-10-204-708-80
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Search completed: December 23, 2004, 19:48:59 Job time : 156 secs

us-10-698-235-1.rnpb

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

120013, 240, App 2147, App 386, App 1670, Ap 28, App 193, App 51, App 51, App 51, App 39, App

Sequence 2147, Ap Sequence 386, App Sequence 1670, Ap Sequence 28, Appl Sequence 38, Appl Sequence 193, App Sequence 193, App Sequence 469, Appl Sequence 39, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 16756, A

US-10-311-455-933 US-10-473-126-240 US-10-311-455-1069 US-10-425-115-120013 US-10-311-455-2147 US-10-311-455-2147 US-10-311-455-2147 US-10-311-455-2147 US-10-311-455-2147 US-10-311-455-2147 US-10-311-455-38 US-10-257-166-38 US-10-257-166-38 US-10-257-166-38 US-10-172-086-51 US-10-172-086-51 US-10-311-507-39 US-10-311-507-39 US-10-311-507-39 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461 US-10-21-174A-461

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Sequence 1, Appli
Sequence 2, Appli
Sequence 386, App
Sequence 122, App
Sequence 252, App
Sequence 1739, App
Sequence 17359,
Sequence 17359,
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                                                                                                                                                               December 23, 2004, 18:16:19; Search time 903 Seconds (without alignments) 10211.434 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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16 US-10-221-613-390

16 US-10-240-589C-122

16 US-10-221-714A-252

8 15 US-10-312-841-1

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17.7 1830121 16 US-10-329-670-1
17.7 1830121 18 US-10-158-865-1
5.7 3673778 15 US-10-312-841-2
5.4 8056 18 US-10-473-126-386
5.3 19380 16 US-10-221-613-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*
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Maximum Match 1008
Listing first 45 summaries
                                                                                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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1656
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19380
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Perfect score:
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ALIGNMENTS

Sequence 1128, Ap Sequence 2128, Ap Sequence 461, App Sequence 461, App Sequence 35, App Sequence 101, App Sequence 17, App Sequence 123, App Sequence 1123, App Sequence 25, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App Sequence 230, App

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Sequence 1, Application US/1032960;

Publication No. US20030099277A1
GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB1661

CURRENT APPLICATION UNBER: US/10/329,960

CURRENT FILING DATE: 2003-01-02

PRIOR APPLICATION NUMBER: US 09/643,990

PRIOR FILING DATE: 2000-08-23

PRIOR PLING DATE: 1995-06-07

PRIOR PLING DATE: 1995-06-07

PRIOR PLING DATE: 1995-06-07

PRIOR PLING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1

SEQ ID NO 1
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a, t, g
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ORGANISM: Haemophilus influenzae
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NAME/KEY: misc feature
LOCATION: (9921). (9921)
OTHER INFORMATION: n equals
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LOCATION: (4747)..(4747
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US-10-329-960-1
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3673778 3683

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NAME/KEY: misc\_feature
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FEATURE:
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FEATURE:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1830121
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US-10-329-670-1

US-110-329-670-1

Sequence 1, Application US/10329670

PUDLICATION NO. US20040018503A1

GENERAL INFORMATION:

APPLICAMY: Flaistchmann et al.

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REFERENCE: PRIAS6P1

CURRENT APPLICATION NUMBER: US/10/329,670

CURRENT FILING DATE: 2002-12-24

PRIOR PILING DATE: 2000-08-23

PRIOR PILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAAAAAAGCGTTAAA 247
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Pred. No. 5.6e-43;
1; Mismatches 57; Indels 1; Ga
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NAME/KEY: misc_feature
LOCATION: (152500)...(152500)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (150841). (150841)
OTHER INFORMATION: n equals a, t,
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t,
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NAME/KRY: misc_feature
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Best Local Similarity 85.1%;
Matches 336; Conservative 1
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LOCATION: (152530)..(152530)
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942158 ATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTATCGTCGAGACATTGGTTACAGGGC 942217 941919 ATATCACAATGGGATCTGCGAGCTTCT-TTAGGTATCGTATTGGCTGCAGAGGGATACCC 941977 942097 942098 IGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAACAAAAAAGCGTTAAA 942157 127 128 GAAAGITITCTTAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGTCG 187 248 ATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTATCGTCGAGACATTGGTTACAGGGC 307 TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAACAAAAAGCGTTAAA 247 308 TGTGGAACGAGAACAAGCAAAATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAAT 367 941978 AAAAGATTATCGCAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 942038 GAAAGTTTTCTTAGCGGGTGTCGCAGAACAAGAAGGCAAGCTAGTCACAAACGGCGGCG 8 ATCACAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGGGATATCC 68 AAAGGATTATCGCAAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 1; Сарв Query Match 17.7%; Score 292.4; DB 16; Length 1830121; Best Local Similarity 85.1%; Pred. No. S.6e-43; Matches 336; Conservative 1; Mismatches 57; Indels 1; Gag 942278 GATGAAATTTAGGAATGAAATTTTAATTAAATTT 942312 368 ATTGTACAGGGTAGAATTGTATTTTCCTAGGATTT 402 U υ ö ö or or or ö ör ö 9 ρ ρ Ø Ø ú ú FEATURE:
NAME/KEY: misc feature
LOCATION: (145942). (145942)
OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc feature
LOCATION: (147197). (147197)
OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc feature
LOCATION: (150841). (150841)
OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, other information: n equals NAME/KEY: misc feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, FEATURE:
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (152530)..(152530) 188 à 셤 ò 셤 ð 셤 8 셤 ò 셤 ò 셤

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RESULT 3

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NAME/KEY: misc feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,t,c, or
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OTHER INFORMATION: n equals a,t,c, or
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NAME/KEX: misc feature
NACATION: (121344)..(121344)
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LOCATION: (100091)...(100091)
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LOCATION: (119750)..(119750)
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LOCATION: (119924)..(119924)
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LOCATION: (120038)..(120038)
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LOCATION: (117136)..(117136)
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LOCATION: (105121)..(105121)
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OTHER INFORMATION: n equals
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LOCATION: (51334)..(51
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10150)..(10150)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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ORGANISM: Haemophilus influenzae
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Sequence 2, Application US/10312841
Publication No. US20030186277A1
Publication No. US20030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC PILE REFERENCE: E01/1208/WO CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
257555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257736 TAİTTATTTİTİTİAATTTTİTTAĞİTİAĞİİAİTTATİTTATİTAİTTTTİTTİTTATTT 257795
                                                                                                                                             308 TGTGGAACGAGAACAAGCAAAATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAAT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901
                                                                                                     942158 ATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTATCGTCGAGACATTGGTTACAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 TCAACTTATGCGACAATTTGTCATCGTAGTATTATATTCTGCAATTCTTCTTTCATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 AGTIGGCGCTTTATTTGCAATAAGTATTGTTGTTAATAATATGTACATTATGCAGTATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGGCTTAACAATGATAGATAAATTCATATATCCATTGTTATTTGGTTTATTTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   842 IGCIGIGITITIAAGITITAAGITITCAIAAAAGAAAAGIATAIAAAACTITCTIGGATTIT
                                                               248 ATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTATCGTCGAGACATTGGTTACAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 GTTTACGATTGCTCTGACAATAAATTAGAATTATTATTTTTTGTTACTTTATGAGGTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 AGTTATTATAGAAATTATTTAATATTTCTAGTATTGAGAGATACACTGAAAGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 GTCTGTTTGTTTGTTTGTTTGTTTTGTTTTTTCAAAATATAGAATTACAAGAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3673778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 94; DB 15; Length 36
46.3%; Pred. No. 3.1e-06;
tive 3; Mismatches 384; Indels
                                                                                                                                                                                                                                                      368 ATTGTACAGGGTAGAATTGTATTTCCTAGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 46.3
Matches 334; Conservative
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; LOCATION: (379615)
US-10-312-841-2
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                                                                                                                                                                                                                                                                                                                                RESULT 4
US-10-312-841-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGGATTATCGCAAAGGCGATGAAATCAGCGGATTGCCTAAAAGTGCGGTCAAAAACGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TGTACTTTGTGTGACTGCGTTAGGCGAAAGTGTATTTGAAGCACAACAAAAAGCGTTAAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                941919 ATATCACAATGGGATCTGCGAGCTTCT-TTAGGTATCGTATTGGCTGCAGAGGATACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ATCACAAATAGSGGATCCACGAGCTTCTATTAGGTATCGTATTGGCTGCAGAGGGATATCC
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llarity 85.1%; Pred. No. 5.6e-43;
Conservative 1; Mismatches 57; Indels 1; Ga
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NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (152500)
OTHER INFORMATION: n equals a,t,c,
              NAME/KEY: misc feature
LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                                                                                                 CATTURE:
NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,t,c,
                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)...(150841)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (131360)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
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Best Local Similarity
Matches 336; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 1472 ATTAAAATAATTAATTAATTAATTAATATAA TAAATATAAAATATAAATTAAA 1530
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                                                                                                                                                               GAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTTGTTAATAATGCAG
                                                                TATACCAATCTTGGATTGGACCTGTTAATTACTCACTTGCATTTAAAGAAATTAATGAGA
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                                                                                                                              775 TAACAAATGCTGGCTTAACAATGATAGATAAATTCATATATCCATTGTTATTTGGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>aaaatrittaaanaaaarratrittaaaaarrataarritaaarritaarritaarrit</u>
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                                                                                                                                                                                                  Sequence 390, Application US/10221613
Publication No. US20040029123A1
GENERAL INFORMATION:
APPLICANT: OLEK, ALGRANGE
APPLICANT: PIEPENBROCK, Christian
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US-10-221-613-390
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 386, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:
CURRENT PELLING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
                                                                                                                                                                                                                   258035 TATTTATTATTATTATTAATGTTTTTATTTATTATGTAATGTAAGTTTTTAGTTATTT 258094
                             1082 TCTTTATCATAAAICTAAGCCTATGAAATCGGGCTCTCCGVAAAATTMARGAATATAAAT 1141
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                                                                                                                            1022 GTTGGGTTATTATAGGACGAATTGTTCCTTATGAGATATTTTCTTTATCTAATATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AAGCGTTAAAATTGGCTGAGCAAATTCAATGGTCTGGGCGTTTTTTATCGTCGAGACATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 5.4%; Score 89.4; DB 18; Length 8056; Il Similarity 44.1%; Pred. No. 2.1e-06; 587; Conservative 3; Mismatches 729; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-10-473-126-386
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                       1008 TCCAATTATTTATCGTTGGGTTATTTTATAGGACGAATTGTTCCTTATGAGATATTTTCT 1067
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US-10-240-589C-122
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APPLICANT: OLEK, Alexander
APPLICANT: PIEBENBROCK, Christian
APPLICANT: BERLIN Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: DNA repair
FILE REFERENCE: 5013.1008
CURRENT APPLICATION NUMBER: US/10/240,589C
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 122, Application US/10240589C
Publication No. US20040076956Al
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.100.130
CURRENT APPLICATION NUMBER: US/10/221,613
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: PCT/EP01/02945
DE 10013047.00
DE 10013047.00
DE 10013047.00
DE 10013043.8
DE 10043056.1
DE 10043056.1
PRIOR FILING DATE: 2001-03-15
2000-04-06
22000-04-07
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Pred. No. 7.6e-06;
1; Mismatches 499; Indels 0;
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Best Local Similarity 43.6%;
Matches 386; Conservative
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; SEQ ID NO 390
r.FNGTH: 19380
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TTTTTCAAAATATAGAATTACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTA--TT
                                                            GTTGTTAATAATGTACATTATGCAGTATACCAATCTTGGATTGGACCTGTTAATTACTCA
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-252
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Publication No. US20040048254A1

GERREAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: EIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with

TITLE OF INVENTION: Diagnosis of Diseases Associated with

TITLE OF INVENTION: Diagnosis of Diseases Associated with

TITLE OF INVENTION: Lumor suppressor genes and oncogenes

FILE REFERENCE: 5013.1005

CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT PILING DATE: 2003-01-21

PRIOR FILING DATE: 2000-03-15

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

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Sequence 1, Application US/10312841
| Publication No. US20030186277A1
| GENERAL INFORMATION:
| APPLICANT: Epigenomics AG | TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC | TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC | TITLE OF INVENTION: UNMBER: US/10/312,841 | CURRENT PILING DATE: 2002-12-30 | NUMBER OF SEQ ID NOS: 2 | SEQ ID NO 1 | LENGTH: 3673778 | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYPE: DNA | TYP
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Pred. No. 0.0001;
0; Mismatches 302;
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Best Local Similarity 48.8%;
Matches 298; Conservative
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APPLICANT: La Royal Thomas J.
APPLICANT: La Royal Thomas J.
APPLICANT: La Royal K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cano, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFREENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 173590
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                                3083 TİTATITIATITITGIGITITITITITİTITITITITITITITITI XITGILITITITITITI 3142
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622 GITTGITTGITTTTCAAATATAGAATTACAAGAATATTAGTTGGCGCTTTATTTGCAA
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5.1%; Score 85; DB 18; Length 11
Best Local Similarity 46.4%; Pred. No. 6.5e-06;
Matches 277; Conservative 0; Mismatches 320; Indels
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OTHER INFORMATION: unsure at all n locations oTHER INFORMATION: Clone ID: MRT4577_89895C.1
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ORGANISM: Zea mays
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US-10-425-115-173590
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NAME/KEY: unsure
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US-10-473-126-339
Sequence 339, Application US/10473126
Sequence 339, Application US/10473126
GENERAL INFORMATION:
TAPPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of interest invention: proliferative disorders
FILE REFERENCE:
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Pred. No. 7.9e-06;
0; Mismatches 334; Indels
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 339
LENGTH: 3683
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ORGANISM: Artificial Sequence
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Best Local Similarity 47.9%;
Matches 312; Conservative
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yihua
APPLICANT: APPLICANT: APPLICANT: Title OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 172177
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                      Gaps
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Pred. No. 8e-06;
0; Mismatches 396; Indels
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US-10-425-115-172717
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Best Local Similarity 45.9%;
Matches 343; Conservative (
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ORGANISM: Zea mays
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342 TTGTTGAATTTAATTAGATAAAAAATATTGTACAGGGTAGAATTGTATTTTCCTAGGATT 401

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Sequence 933, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT PILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DET/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
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SEQ ID NO 933
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                 5.1%;
al Similarity 46.0%;
562; Conservative
                                                                                                                   Query Match
Best Local Similarity
Matches 562; Conserv
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                                                                     Score 84.2; DB 15; Length 6255;
Pred. No. 1.8e-05;
0; Mismatches 423; Indels 1;
                       ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA
US-10-311-455-933
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                     Query Match 5.1%;
Best Local Similarity 45.1%;
Matches 349; Conservative
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1616 2332 2272 2212 2152 2035 1975 1916 1856 1037 1796 1094 1154 1214 1275 CTAACAGCAATTCTTTACCAATGTTTTTTAATGCAATYCCTTAYCCAAATGGAATACAA 1334 8 2092 1736 TIAGATAGCITAAAATATAAATCAGGAGCTCTTGTTGGTAAAACTTATTCAGGAGGAAAG 1274 irtradadırırdadari randarırı radarı -- Arradarır radradırı radırı 1558 917 502 562 617 677 716 737 GTTAATTACTCACTTGCATTTAAAGAAATTAATGAGATAACAAATGCTGGCTTAACAATG 797 857 TAA---TATTTCTAGTATTGAGAGATACACTGAAAGT--TATTTGTCTGTTTGTTT 2151 TTTATTTAATAAATAAAATTATTAAAATTATATAAATTAAATAATTAATT 858 TTAAGTTTCATAAAAGAAAAGTATATAAACTTTCTTGGATTTTTGACTTTTATTTTTTA 918 GCTGTGATGTATGTTTTTTTTCGAGCGTATACAACAAAATCCCATGAGCGTTTTATT TTTTTTTTTTTTTTTTAAACGAAATTTTATTTTTTTTTAAATTAAATTAAATA ---GGACGAATTGTTCCTTATGAGATATTTTCTTTATCTAATATTCCTCTTTATCATAAA TCTAAGCCTATGAAATCGGGCTCTCCGVAAAATTMARGAATATAATTTTAATTAATGGGG GAAAGTGCGACCTCAAGTCATTTTAGTGCTTTTGGTTACGGGAGAAAAACATCTCCTTTT 1675 AATTTTATCGTATTAATTAAAATTTTTTTTTTAATTTTACGATTCGTTTATTTCGATTT 443 AAATTAGAATTATTATTTTTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTGT 2271 Traarriatriaaaratariaaaaraaaritrrarraaaaritaaarriritririri 618 GTTTGTTTGTTTGTTTTCAAAATATAGAATTACAAGAATATTAGTTGGCGCTTTATTT ATAGATAAATTCATATACCATTGTTATTTGGTTTATTTGAAGTTGCTGTGTTTTTAAGT GCAATAAGTATTGTTAATAATGTACATTATGCAGTATACCAATCTTGGATTGGACCT 19; ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-240 8056 Length Indele Score 83.8; DB 18; Pred. No. 2.3e-05; 4; Mismatches 638; CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056 1215 1615 g g à 8

cell

Sequence 240, Application US/10473126
PUblication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic;
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:

757

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7222 TTAŤTTÅGÅÅGGGTATGAATÁTAŤATÁTGGATATÁTTŤATŤTTAAŤTTTATÅGGATT 7281
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                                                                                                       AAATATAGAATTACAAGAATATTAGTTGGCGCTTTTATTTGCAATAAGTATTGTTGTTAAT
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Publication No. US20040023330A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of

TITLE OF INVENTION WHERE: US/10/257,166

CURRENT APPLICANTION NUMBER: US/10/257,166

CURRENT PILENG DATE: 2002-10-07

PRIOR APPLICATION NUMBER: PCT/EP01/07470

DE 10032529.7

PRIOR APPLICATION NUMBER: PCT/EP01/07470

PRIOR APPLICATION NUMBER: 2001-06-29

PRIOR PILING DATE: 2001-06-29
                                                           1557 AAAAAATAATTTTTATTTAAAAATTTTTTAACGTATTT--ATATTTTATATTTATAT 1500
                                  CAGATAGCTAAAGGAGATACGAATTTATTTAATTTAGCGAAAGAGCAAGGCTTTCAGACA 1394
                                                                                                                                        1452 GCTTGGATTGATGATATTCGTTTTCCAGATAATGAAGGGTATTCTTTAAGAGATTCAATG 1511
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                                                                                                     1395 TATTITIATICAGCICAAGCIAGGATGATAIGCATAI---GAICAATTITIAGGAGGA
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 178
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LENGTH: 8776
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                         Run on:
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|         | ion                                     | Mus muscu | CH216-165 | CH261-180 | CH216-151 | ISB1-1230 | CH216-143 | CH216-151 | CH216-159 | AGENCOURT | Mus muscu | ISB1-2H14 | CH216-46A | CH216-165 | P042-2-C1 | CH216-167 | P053-3-B1 | CH216-165 | Drosophil | SP Ba006 | P053-1-D0 | HS 3153 A | Mus muscu | Drosophil | P048-4-G0 |
|---------|---|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|
|         | Description                             | AG349719  | CL081966  | CC253231  | CL078538  | CL143963  | CL077122  | CL078589  | CL080711  | CF238805  | AG386981  | CL083840  | CL038406  | CL082000  | CG748432  | CL082569  | CG758143  | CL081992  | AL069706  | BZ695529 | CG757757  | AQ897537  | AG347262  | AL063921  | CG753732  |
|         | 1 |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |          |           |           |           |           |           |
|         | qı                                      | AG349719  | CL081966  | CC253231  | CL078538  | CL143963  | CL077122  | CL078589  | CL080711  | CF238805  | AG386981  | CL083840  | CL038406  | CL082000  | CG748432  | CL082569  | CG758143  | CL081992  | CNSOOEVL  | BZ695529 | CG757757  | AQ897537  | AG347262  | CNS0039G  | CG753732  |
|         | : :                                     | 6         | 0         | 8         | 0         | 6         | 9         | 6         | 6         | 9         | 6<br>6    | 0         | 6         | 9         | 9         | 6         | 6         | 6         | 6         | В<br>В   | 6         | 8<br>A    | 6<br>4    | 6         | 6         |
|         | Match Length DB                         | 1254      | 2157      | 1277      | 1536      | 1205      | 1162      | 1493      | 1805      | 1626      | 1542      | 1599      | 1594      | 1981      | 1344      | 1632      | 1297      | 1784      | 1101      | 1206     | 1566      | 1139      | 1638      | 1101      | 1811      |
| م<br>ما | Match                                   | 6.5       | 6.3       | 6.2       | 6.2       | 6.2       | 6.2       | 6.2       | 6.2       | 6.1       | 6.1       | 6.0       | 6.0       | 6.0       | 5.9       | 5.9       | 5.9       | 5.9       | 5.9       | 5.9      | 5.9       | 5.9       | 5.9       | 5.8       | 5.8       |
|         | Score                                   | 107.8     | 103.8     | 103.2     | 102.8     | 102.6     | 102.4     | 102.2     | 102       | 101.4     | 101.2     | 8.66      | 66        | 98.6      | 98.4      | 98.4      | 98        | 86        | 97.8      | 97.6     | 97.6      | 97.2      | 97        | 96.8      | 96.6      |
| Result  | No.                                     | -         | 7         | с<br>3    | C 4       | υ<br>O    | 9<br>U    | 0 7       | 8         | ი<br>ს    | 10        | c 11      | c 12      | 13        | 14        | c 15      | 16        | c 17      | c 18      | 19       | 20        | 21        | 22        | c 23      | 24        |

| AG370846 Mus muscu<br>CL082685 CH216-169<br>CG757503 PO52-4-C0<br>BE420745 HWM002.B0<br>CR722884 Tetraodon<br>AG376784 Mus muscu<br>AL298972 Tetraodon<br>AG33167 Mus muscu<br>CG745119 PO37-4-G0<br>CL461494 SALL 1148<br>AL226115 Tetraodon<br>AJ592026 Arabidops<br>CL503354 SALL 811<br>BZ696936 SP Ba009<br>AG347097 Mus muscu<br>CG78412 CH216-151<br>AG382256 Mus muscu<br>AG346348 Mus muscu<br>AG346348 Mus muscu<br>AG346348 Mus muscu | ALIGNMENTS  AG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719  MAG149719.1 G1:4792302  MAG149719.1 G1:4792302  MA |
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| AG370846<br>CL082685<br>CG757503<br>BE420745<br>CR722884<br>AG376784<br>AG376784<br>CCS745119<br>CC745119<br>CC745119<br>CC749499<br>CC749499<br>CC749499<br>CC749499<br>AG386256<br>AG346348<br>AG346346  | lus molossinus DNA, lus molossinus DNA, lus molossinus DNA, lus molossinus lus molossinus lus molossinus i, Metazoa, Chordata, Eutheria; Rodentia; i, Metazoa, Chordata, lus molossinus i, Metazoa, Chordata, lus molossinus i, Metazoa, Chordata, lus molossinus lus molossinus i, Metazoa, Chordata, lus molossinus lus molossinus lus exerches of Library luc 1254) cal Research (RIKEN) lus es |
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Applibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.

    Cases 1 to 2157)

                                                    I. (bases 1 to 2157)

Wardis, E. and Wilson, T. McPherson, J., Warren, W., Graves, T., Wardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)

Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 17500 Std Brror: 0.00
Seq primer: Sp5 atcrgcgtttcgatcct
Class: BAC ends
High quality sequence stert: 341
High quality sequence step: 412.

I. 2157

Location/Qualifiers
II. 2157

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/dlone="CH216-165D13"
/sex="male"
/clone="CH216-165D13"
/coll | Insert Laxon: 8364"
/clone="CH216-165D13"
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                                  Length 1254;
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                               6.5%; Score 107.8; DB 9;
.larity 47.4%; Pred. No. 5.4e-10;
Conservative 0; Mismatches 427;
                                              Best Local Similarity
Matches 390; Conserv
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                                Query Match
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/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTTGTTAATAATGTACATT
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                                                                                                                      Query Match 6.3%; Score 103.8; DB 9;
Best Local Similarity 47.8%; Pred. No. 3e-09;
Matches 427; Conservative 0; Mismatches 458;
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Xenopus tropicalis (western clawed frog) Xenopus tropicalis

GSS.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

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                                TAAATTAGAATTATTATTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTG
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CH261-180N11 RM1.1 CH261 Gallus gallus genomic clone CH261-180N11,
genomic survey sequence.
                                                                                                    1064
                                                                                                                            ICTTTATCTAATATTCCTCTTTATCATAAATCTAAGCCTATGAAATCGGGCTCTCCGVAA 1124
                                                                                                                                                                                                        1125 AATIWARGAATATAATITTAATIGGGGGAAAGTGCGACCTCAAGTCATITTAGTGCT 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1277)

Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

Gallus gallus BAC End Reads

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                    1005 AAATCCAATTATTTATCGTTGGGTTATTTTATAGGACGAATTGTTCCTTATGAGATATTT
                                                                                                                                                                                                                                                                            AAGCAAAATAGTTAGAAATCTTGTTGAATTTTAATTAGATAAAAATATTGTACAGGGTAG
                                945 GCGTATACAAAAATCCCATGAGCGTTTTATTTCACCTAACACTGTTTATTCTCGATTA
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                                                                                                                                                                                                                                                                                                                                1984 TITITALGATITATIAATAATATICIIGIATATATATATITITITITITANAITA 2037
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.larity 45.7%; Pred. No. 3.9e-09;
Conservative 2; Mismatches 556; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wstl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="UCD001, inbred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="CH261-180N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC253231
CC253231.1 GI:30589981
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IGTTATTTGGTTTATTTGAAGTTGCTGTGTTTTTAAGTTTTAAGTTTTCATAAAAAGAAAAG 879
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Pred. No. 5e-09;
2; Mismatches 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wateon.wuetl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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High quality sequence stop: 664.
Location/Qualifiers
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CL143963/c
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                                                            SM Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

E (bases 1 to 1536)

Kremitzki,C., Caraniata; Vertebrata; Euteleostomi;

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

L Unpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 175000

Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 ICTIGITGAATTIAATTAGATAAAAAATATTGTACAGGGTAGAATTGTATTTTCCTAGGA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 CIGCAATICTICTITCATIAGAAGTIATTATAGAAAATTATTAATATTTCTAGTATTG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 AATATAGAATTACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTTGTTAATA 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    700 AIGTACATTAIGCAGTATACCAAICTIGGATIGGACCTGTTAATTACTCACTIGCATTTA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 TITAGGAITITGITAGGGCAACGITTACGAITGCICTGACAATAAAITAGAAITAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 TTTGTTACTTTATGAGGTTATACAACTTATGCGACAATTTGTCATCGTAGTATTATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 1536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 102.8; DB 9;
ilarity 46.2%; Pred. No. 4.6e-09;
Conservative 0; Mismatches 402;
                                                                                                                                                                                                                                                                                                                                                                                                                               1. 1536
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-151C11"
CH216-151C11, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                          Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 1061
High quality sequence stop: 1145.
Location/Qualifiers
                 CL078538
CL078538.1 GI:40534451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346;
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Best Local 8
           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Matches
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AUTHORS
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1205 bp DNA linear GSS 05-JAN-2004 ISB1-12302 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-12302, genomic survey sequence. 1143 1083 1000 GATTAAAATCCAATTATTTATCGTTGGGTTATTTTATAGGACGAATTGTTCCTTATGAGA 1059 ï 488 548 608 666 Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases I to 1205)
Kremitzki, C. (arter, J. McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson BAC 940 TICGAGCGIATACAACAAAAICCCATGAGCGITTTATTTCACCTAACACTGTTTATTCTC 489 ATGCGACAATTTGTCATCGTAGTATTATATTCTGCAATTCTTCTTTCATTAGAAGTTATT 1142 TİTTATTATITITITATNITATAAİTATITITITITITITATATITITITITITATATITİ Gapa /organism="Xenopus tropicalis"
/mol Lype="Uganomic DNA"
/db zref="texon:8364"
/clone="ISB1-12302"
/clone\_lbe="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"

503

563 941 623 881 683 821 743 761 803 701 863 641 923

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CL078589 1493 bp DNA linear GSS 31-DEC-2003 CH216-151KS Sp5.1 CH216 Xenopus tropicalis genomic clone CH216-151KS, genomic survey sequence.
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/cell_line="Stock 248 F7A2, inbred N7"
/clone_li1="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                   444 AATTAGAATTATTATTTTTTTTTATTGAGGTTATATCAACTTATGCGACAATTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGITITITITITICAAAATATAGAATTACAAGAATATTAGTTGGCGCTTTATTTGCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 AGTATTGTTGATAATGTACATTATGCAGTATACCAATCTTGGATTGGACCTGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 TACTCACTTGCATTTAAAGAAATTAATGAGATAACAAATGCTGGCTTAACAATGATAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCATAAAAAGAAAAGTATATAAACTTTTCTTGGATTTTTTGACTTTTATTTTTTATGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      984 AACACTGTTTATTCTCGATTAAAATCCAATTATTTATCGTTGGGTTATTTTATAGGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 AAATTCATATATCCATTGTTATTTGGTTTATTTGAAGTTGCTGTGTTTTTAAGTTTAAAGT
                                                                                                                                                                                                                                                                                                                                                         TIGIALTITICCTAGGATTITAGGATTITIGTTAGGGCAACGTTTACGATTIGCTCTGACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 ATCGTAGTATTATATTCTGCAATTCTTCATTAGAAGTTATTATAGAAAATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        924 ATGATGTATGTTTTTTTTGAGGGTATACAACAAAATCCCATGAGGGTTTTTATTTCACCT
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Pred. No. 5.5e-09;
0; Mismatches 377;
                               1. .1162
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/db_xref="taxon:8364"
/clone="CH216-143E5"
High quality sequence stop: 808.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 328; Conserva
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 605
                                                                                                             GCTTTATTTGCAATAAGTATTGTTGTTAATATGTACATTATGCAGTATACCAATCTTGG 728
                                                                                                                                                  729 ATTGGACCTGTTAATTACTCACTTGCATTTAAAGAAATTAAATGAGATAACAAATGCTGGC 788
                                                                                                                                                                                                                        TTAACAATGATAGATAAATTCATATATCCATTGTTATTTGGTTTATTTGAAGTTGCTGTG 848
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                                                                          TGTTTGTTTGTTTGTTTGTTTTTCAAATATAGAATTACAAGAATATTAGTTGGC
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

I (basea I to 1162)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
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Mashington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 757
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Xenopus tropicalis
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CL077122/c
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Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Xenopus; Tropicalis genome

Lopublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                         CL080711 1805 bp DNA linear GSS 31-DEC-2003 CH216-15918 RM4.1 CH216 Xenopus tropicalis genomic clone CH216-15918, genomic survey sequence.
                                                                                                                                                       987 ACTGTTTATTCTCGATTAAAATCCAATTATTTATCGTTGGGTTATTTTATAGGACGAATT 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                       909
                                                                  927 ATGTATGTTTTTGTTCGAGCGTATACAACAAAATCCCATGAGCGTTTTATTTCACCTAAC 986
                                                                                                                                                                                                 329 ATAGTTAGAAATCTTGTTGAATTTAATTAGATAAAAATATTGTACAGGGTAGAATTGTA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell line="Stock 248 F7A2, inbred N7"
/clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
449 GAATTATTATTTTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTGTCATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 TTTTCCTAGGATTTAGGATTTTGTTAGGGCAACGTTTACGATTGCTCTGACAATAAATTA
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Best Local Similarity 43.3%; Pred. No. 6.5e-09;
Matches 546; Conservative 4; Mismatches 706; Indele
                                                                                                                                                                                                                                            1047 GTTCCTTATGAGATATTTTCTTTATCTAATATTCCTCTTTAT 1088
                                                                                                                                                                                                                                                                                      485 NİTTITITITITITİTİTİTİTİTİTİTITİTİTİTİTİ
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/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-15918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM4 ctcaagggcatcggtcgagc
Class: BAC ends
High quality sequence start: 690
High quality sequence stop: 766.
Location/Qualiflers
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CL080711.1 GI:40536624
GSS.
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KEYWORDS
SOURCE
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibiae; Menopus; Silurana.

( Dases 1 to 1493)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Aphysical map of the xenopus tropicalis genome Unpublished (2003)

Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Pred. No. 6e-09;
                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Mashington University School of Medicine
Baall: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
                                                           Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-151K5"
                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends
High quality sequence start: 1009
High quality sequence stop: 1070.
Location/Qualifiers
                    CL078589.1 GI:40534502
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                                                        CF238805 16099447 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone IMAGE:6995950 5', mRNA sequence.
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/lab host="DH10B (phage-resistant)"
/clone lib="NUHD XGC Embs"
/note="Vector: pGWv-SFORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
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I (Bases 1 to 1626)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAny Bethesda, MD 20892
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation. Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM14680 row: g column: 21
High quality sequence steart: 71
High quality sequence stop: 316.
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/clone="IMAGE:695950"
/tissue_type="neurula"
                                                                                                                                                                                            CF238805.1 GI:33442013
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         AG386981 1542 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-201G10.TJ, genomic survey
                                                      AG386981.1 GI:47998186 GSS.
Mus musculus molossinus
                                    seguence.
                     DEFINITION
                                           ACCESSION
                                                      VERSION
KEYWORDS
SOURCE
AG386981
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehirro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, Wit.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170] (Thome are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 phone; 81-298-36-9189, fax: 81-298-36-9199 392 752 838 479 452 539 512 540 TTTTATATTATTATTATTATATATATATTTTTTATTTTTAATAATTAATTAATTAATA 599 572 658 718 692 778 632 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. TTATATTCTGCAATTCTTCTTTCATTAGAAGTTATTTATAGAAAATTATTTAATATTTCT TITICAAAATATAGAATTACAAGAATATTAGTTGGCGCTTTATTTGCAATAAGTATTGTT 779 TTTTTTATTTTTTTATTTTTTTTTTATTATTTATTTAATTAATTTAATTTATTATTATT 333 TTAGAAATCTTGTTGAATTAAATTAGATAAAAAATATTGTACAGGGTAGAATTGTATTTT 393 CCTAGGATTTAGGATTTTGTTAGGGCAACGTTTACGATTGCTCTGACAATAAATTAGAAT TATTATTTTTTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTGTCATCGTAGTA GITAATAATGTACATTATGCAGTATACCAATCTTGGATTGGACCTGTTAATTACTCACTT Gape Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. BAC end Sequences of Library MSMg01 Unpublished 2 (bases 1 to 1542) Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. Direct Submission 3, Length 1542; /ecx="male" /tissue\_type="mixture of kidney and spleen" /clone\_lib="MSMg01 Mouse Male BAC Library" Indele Location/Qualifiers 1. .1542 /organism="Mus musculus molossinus" Query Match 6.1%; Score 101.2; DB 9; Best Local Similarity 44.4%; Pred. No. 9.2e-09; Matches 439; Conservative 3; Mismatches 544; /mol\_type="genomic DNA" /sub\_species="molossinus" /db\_xref="taxon:57486" /clone="MSMg01-201G10.TJ" e-mail: abe@rtc.riken.jp musculus molossinus : pBACe3.6 : EcoRI : ECORI Sequencing : TJ LIBRARY Vector R.Site 1 R.Site 2 PRIMERS 453 513 633 REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES ò

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Sanopus; Silurana.

(bases 1 to 1594)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
             /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
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Matches 326; Conservative
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Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wastson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
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|mol_type="genomic DNA"
|db_xref="taxon:8364"
|clone="ISB1-2H14"
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CL083840/c
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1044 ATTGTTCCTTATGAGATATTTTCTTTATCTAATATTCCTCTTTATCATAAATCT 1097
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CL082000.1 GI:40537913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3AC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.23
Matches 326; Conservative
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                                                                                                                                                                                                                                                 /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Pred. No. 2.4e-08;
0; Mismatches 387; Indels
A physical map of the xenopus tropicalis genome Unpublished (2003)
                                  Genome Sequencing Center
Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Length: 175000 Std Brror: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ands
High quality sequence start: 471
High quality sequence stop: 522.
Location/Qualifiers
                                                                                                                                                                  /organism="xenopus tropicalis"
/wol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8164"
/clone="CH16-4666"
                          Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.8%;
Matches 327; Conservative
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CL082000 1981 bp DNA linear GSS 31-DEC-2003 CH216-165P18 RM4.1 CH216 Xenopus tropicalis genomic clone CH216-165P18, genomic survey sequence.
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                                                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1981)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 AATTAGAATTATTATTTTTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTGTC
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46.2%; Pred. No. 2.8e-08;
tive 0; Mismatches 379; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM4 ctcaagggcatcggtcgagc
Class: BAC ends
High quality sequence start: 265
High quality sequence stop: 497.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-165P18"
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786

498 999

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Second tropicalis (western clawed frog)

Second tropicalis (western clawed frog)

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Kenopodinae; Xenopus; Silurana.

El (Masse I to 1632)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 175000

Seq primer: Sp6 ArTTAGGTGACACTATAG

Class: BAC ends

High quality sequence start: 1062
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679 CAATAAGTATTGTTGTTAATAATGTACATTATGCAGTATACCAATCTTGGATTGGACCTG 738
                                                                                                  TIGICATCGIAGIATIATATICTCCAATICTTCTTTCATIAGAAGTTATATAGAAAT
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                                                                                                                                                                     TTAATTACTCACTTGCATTTAAAGAAATTAATGAGATAACAAATGCTGGCTTAACAATGA
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                                                                                                                                TAGATAAATTCATATATCCATTGTTATTTGGTTTATTTGAAGTTGCTGTGTTTTTAAGTT
                                 CAATAAATTAGAATTATTATTTTTTTTTATCATTATGAGGTTATCAACTTATGCGACAAT
                                                                 607 NITITITITITITITITITITITITITITITITINNITITITITITITITITITITITITITITIT
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CH216-167PS_Sp6.1 CH216 Xenopus tropion (CH216-167PS) genomic survey sequence.
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CL082569.1 GI:40538482
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Srinhivasan,J., Sinzyw., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Srinhivasan,J., and der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                        984 AACACTGTTTATTCTCGATTAAAATCCAATTATTTATCGTTGGGTTATTTTATAGGACGA 1043
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BAC Library Pristionchus pacificus genomic,
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                                                                 AAATTCATATATCCATTGTTATTTGGTTTATTTGAAGTTGCTGTGTTTTAAGTTTAAGT
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/note="The library was generated by a partial digest
the genomic DNA with EcoR! and cloning into the BAC
vector."
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                         1044 ATTGTTCCTTATGAGATATTTTCTTTATCTAATATTCCTCTTTAT 1088
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannatr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
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Organiem="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="california"
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Class: BAC ends.
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                                                                                                /sex="male"
/coll_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                  448 AGAATTATTATTTTGTTACTTTATGAGGTTATATCAACTTATGCGACAATTTGTCATCG
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                                                                                                                                                                                    Score 98.4; DB 9; Length 1632;
Pred. No. 3e-08;
0; Mismatches 418; Indels
ality sequence stop: 1114.
Location/Qualifiers
1. 1632
/organism="Xenopus tropicalis"
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/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="1216-16795"
                                                                                                                                                                                   5.9%;
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